

2 32
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG
arg val asn arg ser arg ser leu ser asn ser asn pro asp ile ser gly thr pro thr

62 92
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC
ser pro asp asp glu val arg ser ile ile gly ser lys gly leu asp arg ser asn ser

122 152
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA
trp val asn thr gly gly pro lys ala ala pro trp gly ser asn pro ser pro ser ala

182 212
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA
glu ser thr gln ala met asp arg ser cys asn arg met ser ser his thr glu thr ser

242 272
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302 332
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp

362 392
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT
ph phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

Cadherin

422 |xxx cleavage xx| 452
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482 512
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542 572
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602 632
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro

1382	1412
GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC	
asp leu ser val leu gln leu asn arg leu leu asp l u l u tyr leu cys val ser cys	
1442	1472
TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA	
phe glu tyr lys gly lys lys val phe gln arg met asn ser leu thr phe lys lys ser	
1502	1532
AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA	
lys asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu	
1562	1592
ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT	
met val arg arg ser arg gly gln leu gln arg ser pro ser gly ser ala phe gly ser	
1622	1652
CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT	
gln glu asn leu arg trp arg lys asp met thr his trp arg gln asn thr glu lys leu	
1682	1712
GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA	
asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu	
1742	1772
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA	
ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu	
1802	1832
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC	
ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn	
1862	1892
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT	
gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe	
1922	1952
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC	
pro glu leu leu phe glu glu glu thr gln gln cys ala asp leu cys leu arg leu leu	
1982	2012
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA	
arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu	
2042	2072
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA	
leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro	

2102 2132
 ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
 met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2162 2192
 TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
 ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2222 2252
 CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
 pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2282 2312
 ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag
 met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2342 2372
 ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
 gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2402 |xxxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxxxxxxxxxxxx
 TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT
 ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val
 xxxxxxxxxxxxxxxxxxxxxxxx|

2492
 GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT
 ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

2522 2552
 CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
 gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2582 2612
 GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
 asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2642 2672 |xxxxx ITAM xxxxx| |xxx
 GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
 glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr

xx ITAM xxx| 2732
 AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT
 lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his

2762 2792
 GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
 gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2822 |xxxxx ITAM xxxx| 2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882 2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu

2942 2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002 3032|xxxxx ITAM xxxx|
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062 3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122 3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182 3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr

3242 3272 |xxxxxxxxxxxxxxxxxxxxxxxxxxxx|
AAG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxx| 3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu

3422 3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his

3482 3512 |xxxxxxxxxxxx|
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys

XXXXXXXXXXXXXXXXXXXXX Coiled coil 2 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser

3602

3632

TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG
ser pro STP

3662

3692

TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC

3722

3752

TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG

3782

3812

TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG

3842

3872

AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG

3902

3932

GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA

3962

3992

CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT

4022

4052

TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG

4082

4112

TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC

4142

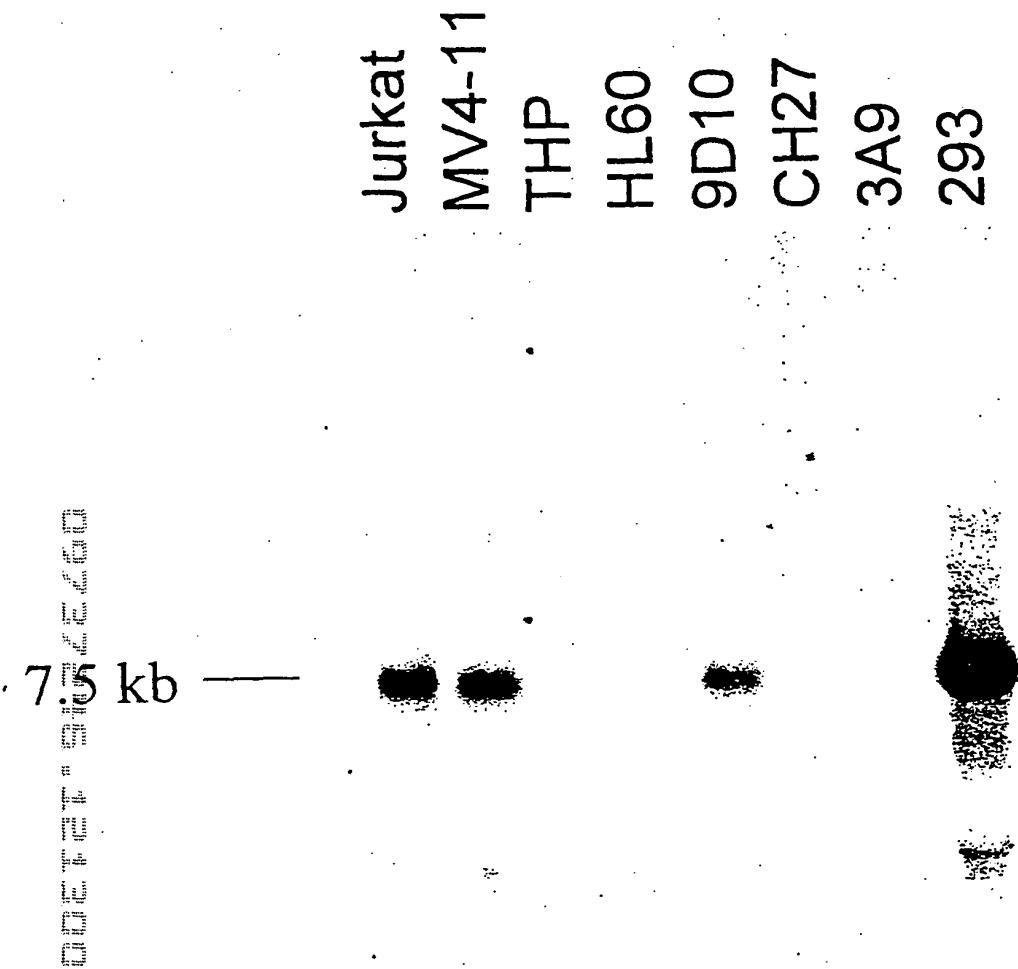
CTC

566 →

PBL
lung
placenta
sm intestine
liver
kidney
spleen
thymus
colon
skel muscle
heart
brain

A

Human CLASP-3 Multiple Cell Lines Northern



HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPFEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPFEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYPELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
KIAA	PVSANLPSGYLGYPELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----GPGPARSTVSISLISNSARV
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A	IIHVVAQCHESHLRSYVKYAYKAEPYVASEYKTVHEELTKILKPSADFLTSTN
KIAA	IIHVVAQCHESHLRSYVKYAYKAEPYVASEYKTVHEELTKILKPSADFLTSTN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5	-----

Cadherin
Cleavage

HC2A	KLLRYSWFFFDVLIKSMQHLIENSKVKLLRNORFPASYHHAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIKSMQHLIENSKVKLLRNORFPASYHHAETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLLLENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIILKSMQHLIDTNKIQLHRPQRFPEYQNELDNLMVLSHDHVIWKYKD
HC3	SALQQAWFFFEIMVKSMVHHLFYNDKLEARRKSRFFPERFMDIAALVSTIASDIVSRFQK
HC5	-----

HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSIASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL
HC3	DTMVERLNTSLAFTLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----

HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY
HC1	QEVCOHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF
HC3	RIICSHHYVTNLNLPCLLTPPASPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA

Cadherin
EC motif

HC2A	CRNHFLVGILLREVGTLQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGILLREVGTLQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGILLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ
HC1	CRKHFLIGILLREVGTFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3	RQQHYLAGLVLTELAVILDPDAEGLFGLHKKVINMVHNLSSHSDSDPRYSDPQIKARVAM
HC5	SSTS-SPGILFTELAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKVCPEVKVKIAA

HC2A	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPLFVGLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPLYGMLLDNMPRIYLDLYPFTVNTSNQGSRDDLTSTNGGFQSQTAIKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIAATDDYESE-----SG---SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

HC2A KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
 KIAA KDLLGAISGIYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
 rat -----
 HC4 TDKDTAYGSFQNG-----HGKREDSRGSLIP-EGATGFPDQNGTGEN-----TRQS
 HC1 KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDDFFTISEVCL
 KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDDFFTISEVCL
 rat -----
 HC4 STRSSVSQYNRLDQYEIRSLMICYLYIVKMISEDTLTYWN-KVSPQELINILILLEVCL
 HC1 ALIGSTLRFDRLDQAETRSLLMCFHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
 HC3 -----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLYLVCV
 HC5 -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFOYMGKRYIARNQEGLG--PIVHDRKS-----QTLFVSRNRTGMM
 KIAA HQFOYMGKRYIAR-----TGM
 rat -----
 HC4 FHFYRMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM
 HC1 QNERYLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
 HC3 SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
 HC5 LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGERGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 rat -----
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
 HC1 QHRSQTLPIIRGK--NALSNPKL--LQMLDNTMTSNEIDIVHHVDTEANIATEGC
 HC3 RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
 KIAA LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
 rat -----KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
 HC4 LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
 HC1 LTILDVLSLFTQTHQRQLQQCDQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC
 HC3 LIILDLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHCFAQRALVS
 HC5 LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCQSTTYLTHCFATLRALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
 rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
 HC4 KFPSAFFKGRVNMCAAFCEYVLKCCCTSKISSTRNEASALLYFLMRNNFEYTKRKTFLRTH
 HC1 KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYFLMRKNFEFNKQKSIVRSH
 HC3 KFPPELLFEEETEQCADLCRLRLRHCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK
 HC5 KFGDLLFEEVEQCFDLCHQVLHHCSSMDVTRSQCATLYLLMRFSFGATS--NFARVK

HC2A LQVVISVSQLIADVVVGIGETRFOQSLSIINNANSRDLIKHTSFSSDVKDLTRIRTVLM
 KIAA LQVVISVSQLIADVVVGIGETRFOQSLSIINNANSRDLIKHTSFSSDVKDLTRIRTVLM
 rat LQVVISLSQLIADVVVGIGETRFOQSLSIINNANSRDLIKHTSFSSDVKDLTRIRTVLM
 HC4 LQIIIAVSQLIADVALSGGSRFQESLFIINNANSRDLIKHTSFSSDVKDLTRIRTVLM
 HC1 LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
 HC3 MQVPMSSLSSLVGTSQNFEEFLRRSLKTIITYAEEDLELRETTFPDQVQDLVFNLMILS
 HC5 MQVTMSLASLVGRAPDFNEEHLRRSLRTIILAYSEEDTAMQMTFPPTQVEELLCNLSILY

Transmembrane

HC2A ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL LSEAAMCYVHV
 KIAA ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL LSEAAMCYVHV
 rat ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL LSEAAMCYVHV
 HC4 ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD MAKIHVKNGL FSEAAMCYVHV
 HC1 ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
 HC3 DTVKMKEHQEDPEMLIDL MYRIAKGYQTS PDLRLTWLQNMAGKHSERSN HAEAAQCLVHS
 HC5 DTVKMREFQEDPEMLMDL MYRIAKSYQAS PDLRLTWLQNM AEKHTKKKY TEAAMCLVHA

domain

SH3

HC2A TALVAEYL TRKGV-----FRQGCTAFRVITPN
 KIAA TALVAEYL TRKEA-----VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
 rat TALVAEYL TRKEAD-----LALQREPPVPFYSHTSCQRKSRGGMFRQGCTAFRVITPN
 HC4 AALVAEFL HRKKL-----FPNGCSAFKKITPN
 HC1 AALIAEYL KRKGYWKVEKICTASLLSEDTHPCDNSNLLTTPSGGSMFSGMWPFLSITPN
 HC3 AALVAEYL SMLD-----RKYLPVGCVTFNISSN
 HC5 AALVAEYL SMLD-----HSYLPVGSVSFNISSN

ITAM

HC2A IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAER YELIADIYKLIPI
 KIAA IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAER YELIADIYKLIPI
 rat IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
 HC4 IDEEGAMKEDAGMMD-----VHYSEEVLLLELLEQCVNGLWKAER YEI ISEISKLI GPI
 HC1 IKEEGAAKEDSGMHD-----TPYNENILVEQLYMCGEFLWKSEYELIADV NKP IIAV
 HC3 VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF MAGMYEAVNEVYKVL IPI
 HC5 VLEESVVS EDTLSPDEGDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEV YKLV IPI

ITAM

ITAM

ITAM

ITAM

HC2A YEKRRD-----
 KIAA YEKRRD FERLAHL YDTI HRAYSKV TEVMHSGRRL LGTY FRV AFFGQAAQYQFTDSETDVE
 rat SMKSGGTLETTHLYDTI HRFYSKV TEVITR-----A-----AGSWDLLPGGLFGQ
 HC4 YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLG-----TFFRVAFY GQ
 HC1 FEKQDFKKLSDLYYD HRSYLKVAEVVNSEKRLFG-----HYRVAFY GQ
 HC3 HEANRDAKKLSTIHGKLQEA FSKIVHQSTGWERMFG-----TYFRVGFY G-
 HC5 LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG-----TYFRVGFY GFG-

ITAM

ITAM

HC2A -FFEDEDGKEYIYKEPKLTP LSEISQRL LKLYSDRFGSENVKMIQDSGKVNPKOLD SKYA
 KIAA GFFEDEDGKEYIYKEPKLTP LSEISQRL LKLYSDRFGSENVKMIQDSGKVNPKOLD SKYA
 rat GFFEDEDGKEYIYKEPKLTP LSEISQRL LKLYSDRFGSENVKMIQDSGKVNPKOLD SKFA
 HC4 SFFEEDGKEYIYKEPKLTGLSEISLRLVKLYGERFGTENVKIIQDSKVNAKELDPKYA
 HC1 GFFEEEEGKEYIYKEPKLTGLSEISQRL LKLYADRFGADNVKIIQDSNKNVNPKOLDPKYA
 HC3 TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA
 HC5 SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGGQFGAEFVEVIKDS TPVDKTKLDPNKA

ITAM

HC2A YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
 KIAA YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
 rat YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA
 HC4 HIQVTVYVKPYFDDKELTERKTEFERHNINISRFVFEAPYTL SGKKQGCIEEQCKRRTILTT
 HC1 YIQVIYVTPFFEEKEIEDRKTD FEMHHNINIRFVFETPFTL SGKKHGGVAEQCKRRTILTT
 HC3 YIQIHYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEQFKRKTILTT
 HC5 YIQIHYVEPYFDEYEMKDRVITYFEKNFNLRFFMYTTPFTLEGRPRGELHEQYRRNTVLT

	Collected	Collected
HC2A	IHCFFPYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFFPYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFFPYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFPYVKKRIPINCEQQINLKF	IDGATDEIKDKTAELOQLCSSTDVDIMQLQLKLQGSV
HC1	SHLFPYVKKRIPVQSQSTELNFI	IEVAIDEMSRKVSSELNQLCTMEEVDIMISLQLKLQGSV
HC3	SHAFPIKTRVNVTHKEEIIILTF	IEVAIEDMKQKTQLAFATHQDPADPKMLQMVLOGSV
HC5	MHAFPIKTRISVIQKEEFVLTF	IEVAIEDMKKKTQLAVAINQEPDPAKMLQMVLOGSV

Continued - Cont 2

HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQFLAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQFLAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQFLAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFIQACSIFLELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQFLDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLC FKDFTKRCEDALRKNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADORE

HC2A	YQEE	MKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMTSS
KIAA	YQEE	MKANYREMAKELSEIMHE	QLG-----
rat	YQEE	MKANYREIRKELSDIIVE	RICPGEDKRATKFPAPHLQRHQRTDNKXHSGRVDQFILS
HC4	YHEGLKSNFRDMVKELSDI	IHE	QILQEDTMHSPWMSNTLHVFCIAISGTSSDRGYGSPRYA
HC1	YQEELRSHYKMDLSELSTVMNE		QITGRDDLK---RGVDQCTTRVISKATPALPTVSISS
HC3	YQRELG----	KLSS	--PZ----
HC5	YQOELKKNYNKLKENLRPMIER		KIPELYKPIFRVESQKRDSFHRSSFRKCETOLSOGSZ-

	SSVVZ
HC2A	SSVVZ
KIAA	
rat	CVTLPEHPHVGTCFVMCKLRRTTFRANHWFCQAQEEAMGNGREKEPWTVI FNSRFYRSWGK
HC4	EVZ
HC1	SAEVZ
HC3	
HC5	

HC2A	-----
KIAA	-----
rat	VH1FF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

C

YIQ+	V	P	D
L			E

B

2 32
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG

62 92
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC

122 152
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA

182 212
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA
met asp arg ser cys asn arg met ser ser his thr glu thr ser

242 272
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302 332
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp
ref 1.1 and 1.2
362 ref 2.1 and 2.2
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

421 452
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482 512
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542 572
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602 632
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro
ref 3.1 and 3.2

662 692
AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG
asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu

722 752
CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT
his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro
ref 4.1 and 4.2

782 812
TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG
ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys

842	872
ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT	TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT
ile ala asn met phe glu leu ser val pro	phe arg gln gln his tyr leu ala gly leu
902	932
GTG TTA ACA GAG CTG GCT GTC ATT TTA gac	cct gat gct gaa gga ctg TTT GGA TTG CAT
val leu thr glu leu ala val ile leu asp	pro asp ala glu gly leu phe gly leu his
962	992
AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA	CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC
lys lys val ile asn met val his asn leu	leu ser ser his asp ser asp pro arg tyr
1022	1052
TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC	ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC
ser asp pro gln ile lys ala arg val ala	met leu tyr leu pro leu ile gly ile ile
1082	1112
ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT	ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA
met glu thr val pro gln leu tyr asp phe	thr glu thr his asn gln arg gly arg pro
1142	1172
ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT	GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT
ile cys ile ala thr asp asp tyr glu ser	glu ser gly ser met ile ser gln thr val
1202	1232
GCC ATG GCA ATC GCA GGG ACA TCG GTG CCT	CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC
ala met ala ile ala gly thr ser val pro	gln leu thr arg pro gly ser phe leu leu
ref5.1 and 5.2	
1262	1292
ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC	TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG
thr ser thr ser gly arg gln his thr thr	phe ser ala glu ser ser arg ser leu leu
1322	1352
ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA	GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA
ile cys leu leu trp val leu lys asn ala	asp glu thr val leu gln lys trp phe thr
1382	1412
GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA	TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
asp leu ser val leu gln leu asn arg leu	leu asp leu leu tyr leu cys val ser cys
1442	1472
TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA	CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
phe glu tyr lys gly lys lys val phe glu	arg met asn ser leu thr phe lys lys ser
1502	1532
AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT	ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
lys asp met arg ala lys leu glu glu ala	ile leu gly ser ile gly ala arg gln glu
ref 6.1 and 6.2	
1562	1592
ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG	AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
met val arg arg ser arg gly gln leu glu	arg ser pro ser gly ser ala phe gly ser
1622	1652
CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG	ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
gln glu asn leu arg trp arg lys asp met	thr his trp arg gln asn thr glu lys leu

1682 1712
GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu

1742 1772
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA
ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu

1802 1832
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC
ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn
ref 7.1 and 7.2

1862 1892
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT
gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe

1922 1952
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC
pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu

1982 2012
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA
arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu

2042 2072
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA
leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro

2102 2132
ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2162 2192
TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2222 2252
CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2282 2312
ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag
met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2342 2372
ggg tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2402 2432
TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT
ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val

2462 2492
GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT
ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

↓ ref 8.1 and 8.2

2552
CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2582 2612
GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2642 2672
GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr

2702 2732
AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT
lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his
↓ ref 9.1

2762 2792
GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2822 2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882 2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu
↓ ref 10.1 and 10.2

2945 2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002 3032
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062 3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122 3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182 3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr

3242 3272
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu
↓ ref 11.1

3302	3332
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC	
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro	
3362	3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG	
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu	
3422	3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT	
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his	
3482	3512
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA	
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys	
3542	3572
AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT	
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser	
3602	3632
TGG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG	
ser pro OCH	
3662	3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC	
3722	3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG	
3782	3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG	
3842	3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG	
3902	3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA	
3962	3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT	
4022	4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG	
4082	4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC	
4142	
CTC	

ref 12.1

Ref 1.1

Sequence of BAC8 using primer C3S3, which spans nucleotides 340-359 of the cDNA. Exon sequence is underlined and represents nucleotides 364-380.

TTTTTTGAATTAATGGTGAGCAAAAAGT GAGCATGTTCTTTAATATTTTTTCTCTTAGTG
AACAAATTTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAAC
GCTTTTCCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGT
GGACACTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTC
TCAGGGATGGTTGCATAAGCTAGCTATATTTTCAAAGGAACTTGTGATACATTCTTTG
CTAGTCATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATAACCAAAGATGG
AAAGAGCTTTATAGATACCCACTGCTATTGTTATGGCTAGTAAACCCTTAGGGAAATG
CCAGTTACAATCAATAAAAAACAACAGTCTGGCTGGGTGCAGTGGCTCACACCTGTA
ATCTCAGCACTTTAGAAGGCCGAGGCAGGAGGATCACTTGAGATCAGGAGTTTGAGAC
GCAGCCTGGGCAACATAGCAAGAGCCCATATNTACCCAAAAAAAATTTTTTTTTTAAAT
TAAGCTAAAACCCTGGNNGGCCACAAAACCTGTAGTTCCCATCTACTTTGGAAAGGCT
TGAAGGANGGGAGGGCTTGCTTTGAGCCCCAAGAANGTTCAAAGGCTNGCNGNCAGG
TTNTGATTCNACACNTGCAACTCCCGCATTGGGTNAAACAAAANCCAAGGAANC.

Ref 1.2

Sequence of BAC9 using primer C3S3, which spans nucleotides 340-359 of the cDNA. Exon sequence is underlined and represents nucleotides 371-380.

AATTAATGGTGAGCAAAAAGT GAGCATGTTCTTTAATATTTTTTCTCTTAGTGAACAAT
TTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAACGCTTTT
CCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGTGGACA
CTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTTCTCAGG
GATGGTTGCATAAGCTAGCTATATTTTCAAAGGAACTTGTGATACATTCTTTGCTAGT
CATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATAACCAAAGATGGAAAGA
GCTTTATAGATACCCACTGCTATTGTTNTGGCTAGTAAACCCTTANGGAAATGCCAGTT
NCAATCAATAAAAAACAACAGTACTGGCTGGGTGCAGTGGCTTACACCTGTAATCTC
AGCACTTTATAAGGCCCNAGGCNNGGAGGATCACTTNAGATCCAGGAGTTTGAGACCAG
CCTGGGCAACATANCAAGAGCCCATATCTACCAAAAAAANTTTTTTTTTTAAATTAAG
CTAAACNCTGGGTGGNACAAACCTGTTNGNTTCCNATNTNCCTTTGGAAAAGCTTANG
AAGGGGAGGGCTTNCTTTGGANCCCCAAAAAGTTNAAAGGGNTTGCAGTCAGCCTTTT
NAATCACCCNNNGGNCCTNTCGCATTGGGATTNCCAANANGCCAANGNAACCCCGNT
CNTNTTTTAAAAAANTNTTTTAAAGNANNTTTNTTNGN

Ref 2.1

Sequence of BAC8 using primer HC3AS7, which spans nucleotides 386-405 of the cDNA. Exon sequence is underlined and represents nucleotides 381-385.

TCTTTNGAAAAAGATTANATTATTAATTCTATGATATATTAACAATACACANCTCTAA
CACTTGGACTATTTTTAAAATATGGCATGTAATTTAATAGATGACTGAAATATTTTAGC
TTCTCAAATATTTTTTAAAGTTCCCTACAATGTTTTGTATTTGCTTAAAATAAAATANA
AAAACCACCATATTACTTTCAGAAAATTATGCTAGCTAACAATAGGACAAAAAATTCT
GTGTATGTCAACAAAAAAATTCAACCTTAAATTTTTTTTTTCCATAAAAAACAGGGC
TACTTGCCAGGTGAGANGTGCTGCCGTATGAGCTCCTCGNTAGATTGCGCNGCCGGA
NTGTCGGNCCCTNCGTTTAATATAACGGCGTGNGCNTGTACCGCAGGCTNTGCTAGGT
CGTGNTCCCAAGATATCNTNTNTANCATANTAGACGNTGGNGNCGNNTGCATGTGGCN
TNATTNTNGCAATTGTNACAATCCTAGTNTGTACNTNANAGNTCNGCCNCTGTGANNT
CGTTGTATAGTCNGNGGCNCGCTTGNTTCTGATGCTGAGAGCANTNNCNNACTNTTNN
NCNCCCATCTTTNCNNTTNNNNNCCCCCNNTTNNATNNTTTNNNTNNCNNNNNNATNT
NTNAANNNACCNC

Ref 2.2

Sequence of BAC9 using primer HC3AS7, which spans nucleotides 386-405 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from HC3AS7 is intron sequence. Additionally, this sequence matches the intron sequence found in the previous sequence (BAC8 sequenced with HC3AS7).

GCGCTNCCNNNTNNTTTATCTTCTGAAAAGACTNATATNATTCTATGATTATAACATTA
CACACTCTAACACTGGACTTNTTAAATATGGATGTAATTAATAGATGACTGAATATTTT
AGCTTCTCAAATATNTTTAANGTCCCTACAATGTTTGNATNTGCTTAAAATAAAATANA
AAACCCCATATTACTTTCAGAAAANTATGCTAGCTAACAATAGGACANAAAAAATTCTG
TGTATGCAACAAAAAAATTCAACCTTNAATCTTCTTTTTTTTCCAATANAAAACAGG
GCTACTCTGCCACAGGCTGGAGTCAGTGGCTGATACAGCTACTGCAGCTCACTCCGGG
CTATGTGATTGCCTGCCTAAGCCTCNGAGTAGTAGGCTCAGGTGCCACTACATGCCAG
TAATCTAAAATTTATAGAGACAGGGCTGCTGTGTGNCCAGGCTGGCTAACTCCGGGCT
AAGCGTTCTTGCCTNGCTCTAAATGTGGGATACAGNATGTATCATNCATCAGCCAAAA
AGTTAATTAANTTCCAGATNANTATTTGCATCAAAGCTCCAATNTAGCTTGAAGTAGA
ACCTGCTCNTTGGCTAGANTATCCCGNNTGTTATGGATCATATTANGCNNTTGTGATGC
CGAATGGNATCTATTCCGGGAGACANATTACTATNGGATGANAGCANATNGCCCNAT
GCTTNTTTGTAACGCTNNANNTAAGAACNTTCTNGACATCGTCATAGNTCGAAGTNNT
NNGCGANTTGATACTAANTTCATGNTANGCCNATGACTNTNGTGATTNNTGANTGNCT
GGGAGAACCTACNTNCCCCNTACNNATANNCTNCACCCCCTACTACTNTNNCNCNTCNC
TCTCTANTTCTACTCCACNTTATTATCCTCNCCTTCNCATCNTCCCATCNTNATTCNAC
GCCNCNANACTTANCNTTNAATNCACTCTNNCT

Ref 3.1

Sequence of BAC8 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-733.

TAATGTACATAGTGCTCATGACTGCAGATGATTTCGTAGAAAATCCAGCCTCAAGGACA
CCAGAACACTGGGATTTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCA
TAAGTAAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCA
AATTAGAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCA
GTATCACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAACTATCAGGTTTACT
GTATAAACATATTTGACTAACCTAAAAGCCACATTCTTGTAATTTCCAATATAGCATCAA
TATTTCTACTTCTCATAAAACAGGGAAAACGTATATCACCAAAAATAACTTCTTATTAC
TTCCTTCTTAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCTGTATTTAT
AATTTGTCTGTTTTCTCAGCAACATCATAAGCTACTTGAGGAGACATACTATAAACTGA
TTTAACAGCTTTAGTGTCCCTACAGCTTAGCTCAATGTTTGACAAATATAGGAGATCAA
TGCTTAAAGGAATAAAGGCCAGGACAAGTTCTGGTAGCAAATAGTCCATAAAAGGTTT
TGGGGGAAAAGGGTAAAAATGGATACATATCGGGGTNGCAAGNTTTTTCCATGTGGG
GTGAGGTGCCCATGCCTT

Ref 3.2

Sequence of BAC9 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-730.

TAACATAGTGCTCTGACTGCAGATGATTTCGTAGAAAATCCAGCCTCAAGGACACCAGA
AACTGGGATTTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCATAAGT
AAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCAAATTA
GAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCAGTATC
ACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAACTATCAGGTTTACTGTATA
AACATATTTGACTAACCTAAAAGCCACATTCTTGTAATTTCCAATATAGCATCAATATTT
CTACTTCTCATAAAACAGGGAAAACGTATNTCACCAAAAATAACTTCTTATTACTTCCT
TCTTAAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCCTGNATTTATAAT
TTGNCTGNTTTTCTCAGCAAACATCATAAGCTACTTGAGGGAGACATACTATTAAACCT
GATTACAGCTTTTANGTGTCCCTACAGCTTAACTCAATGTTTTGCAAAATNTNNGGAGA
TCAATGGCTTTAAAGAATAAAAGANCAGGGACAAGTTNTGGGTNGCCATNAGNACAA
TAAAGGTTTTNNGGGGAAAAGGGGAAAAAATNGATTNCATNTCGNNGTTNGCAAGGTN
TTTTCCATTGNGGGGNGGAGGGGCCCATGCCATAANTTTTAACCTTTCTTTTTTNGAAG
AAATTAAACNNTTAAAGGGGTN

Ref 4.1

Sequence of BAC8 using primer HC3AS6, which spans nucleotides 924-944 of the cDNA. Exon sequence is underlined and represents nucleotides 802-917.

CCAGTCTGCAATATGCTGTGCGAAGCCGATATCAACTTTGCATCTTTGTCTTGNCATTC
GAGAAATCAGACTTGTGGAAGTAGGAGACAGCTTACAGCGTGCACAAGCTCTCAGCA
 GAGCATATACGAATGAATCTTTTCCAGGGAGTTATTTATATACTACCTGAGCAAGCCA
 CTTTAGCTTTGGGCAGGAACCTTNTGGATGTTATAAGTAATACTTATATGAATAATATGA
 AATTAATATTTACTTCTTTTACANTCTTCTCTTTTCCTTATCTTAGCCTTTATCCCCTTGT
 GGAAAAGACACTATCAATGCTAGATNCTCCCAAGNCAGAGAATTATGCAGGTTTGGTC
 AGAGAATCGACACAGACATGTTTACAGATTCTTCTTGAAATACATATTGTGCACGAGT
 TTTTACANTATCTCAATTTAGATCTCAGACAGCATNTNGACTAGNGGGTCTAGGACAT
 AGATACATNTTTGNGAACTTCTATAGAANAACNTNTGCNTTAAAAAGGAGCTTGTTNG
 ANANGAATNNNCTGNGAAGGGCCCCGATACGANAATTTGACTTCGGNGAAAATTNNNG
 GATTNNTACAAANTTCTAGGNGGCACCTTNAANAANGNNTGGGNACNTTGGNGGCGGA
 AAAAAAGCCCTTCNTTTAGNTNTCCCGAAATGGAAAAGTNCCAANTTCCNAAAAAA
 ANGGGCTTTGTTNNCTTNCNANA

Ref 4.2

Sequence of BAC9 using primer HC3AS6, which spans nucleotides 924-944 of the cDNA. Exon sequence is underlined and represents nucleotides 802-921.

GACGCCAGCTCTGTACACAGTCTGCAATATGCTGTGCGAAGGCCGATATCAACTATT
GCATCTTTGTCTNGNCATCGAGAAATCAGACTCTGTGGAAGNAGGCAGACAAGACTAT
 ACAGCNTGCACANAGCATCTCAGCAGGCATATAAGAATGAANCTTTTCCAGGGAGTTA
 TTTATATACTACCTGAGCAAGNACTTCAACTTNGGCAGGAACCTTGTGGATGNTTATAA
 GTATACTTATATGAATAANATNGAAATTAATATTTAATTCTTTTACTTCTTCTTTTCC
 TTATCTTAGCCTTTATCCCCTCGTGAAAAAGAGCACTAATCAATGCTATTNCTNCCAAG
 NCAGGAATTTATAGCAGGTTGGTCGAGAATCGACACGACATGTTTACAGANTCATCTT
 GAATACATNATTGTGCACGAGTNTTTTACTCTATCTCAAAATATAGATCTCAGATCGTC
 TATNGANTATGNGGTTCTAGGACATGATTACATTTTNGGGAACTTCCATAGAATAAA
 CNTNTACCTNAAAANANGAGCCTGTTNGAAATNGAATCTACTNCTAAAGGGCNAAGTNC
 CANATTTTACTTCCGCGANATNTCNGGATGTTACAAGTCTAGGGGGNCTTTAGNACGT
 TNGATNTTTGANCGGAAAAAAGCCCTTCTANNGGTCNCCTAATGGAAGCGCCAATTCC
 NAANAAGGNCTGTGTTNTTNGACATTTACCNNGNCCNTTTCTAATCAAACNTNCTCTTC
 TNNNANCCNCANCNCNNNCCTATANNCCCTATCNCTCNNCTNNNCTCNTCACTCTCNNG
 NCTNTCTTCCNTTCTNCACTNTNNNNTCNCTNNNATNNNCTTCTCCNATCCNTCTCANN
 NNNTCANNCTCCCTACNNTNCNCNTNTTACCATCTNCNCCNNCCT

Ref 5.1

Sequence of BAC8 using primer C3S6, which spans nucleotides 1127-1146 of the cDNA. Exon sequence is underlined and represents nucleotides 1181-1269.

GTATGATCCGCCAGACCGCTGCCATGGCAATNGTAGGGACATCGGTCCCTCAACTAAC
AAGGCCTGGCAGTTTCCTNCTCACGTCAACGGTCAAAACAATCCTTCTACAGAATTTT

TTTTCTNGAAAGACAAATATTTACTAGGATATGCCCTTAAATATATGAGATGATTGTAT
 CAGCTGATGCAAAAAGTGCTCAGTTTTATTTATGAAAATATTAAGTTCCCAGAATATTA
 ACTGTCTTCTCCCAAACAGTTTTAAAAAATGATTACCTCAAGGTTTATGGGAAAAAGC
 CCCGTATTCTGCATTGAGAAATTTGGAAAATTGCCTCATTATAGATAGCCATNTCTTTTTT
 TTNTTTTTTTTTATNCTTCAAGTCTTAGGGNACATGTGCACAACATGCAGGNTAGTTACA
 TATGTATACATGTGCCATGTTGGTGTGCTGCACCCANNAACCCGCAATTTAACATTAGG
 TNTATCTCCAAATGCTATCCNTTACCCTTCCCCCATNCCACAACAAGGCCCCGGGCNT
 TGNGATGTTCCCTTCTGTGCCCACTGTGTNTCACATTNCCNCTTCCCNCCCTTANTN
 NNGTGCAGAACNTNGCCNGTNGCCCTNTNTTTTTTNNCCC

Ref 5.2

Sequence of BAC9 using primer C3S6, which spans nucleotides 1127-1146 of the cDNA. Exon sequence is underlined and represents nucleotides 1151-1269.

CCNCTGATGATTATGAAAGTGAGAGCGGAAGTATGATAAGCCAGACCGTTGCCATGGC
AATCGCAGGGACATCGGTCCCTCAACTAACAAGGCCTGGCAGTTTCCTCCTCACGTCA
ACGGTAAAAACAATCCTCCTACAGAATTTTTTTTTCTAGAAAGACAAATATTTACTAGG
 ATATGCCCTTAAATATATGAGATGATTGTATCAGCTTGATGCAAAAAGTGCTCAGGTTT
 ATTTATGAAAATATTAAGTTCCAGAATATTTAACTGTCTTCTCCCAACAGTTTTAAAA
 AATGATACCTCAGGTTTATGGGGAAAAAAGCCCCGTATTCTGTCATTCAGAAATTTGG
 AAAATTTGNCTCATTATAGATAGTTCATTTTCTTTTTTTTTTTTTTTTATACNTTTAA
 AGTTTTTAAGGGGNACCATGTTGCACCAAANATTGCAGGGGTTNGGTTACCATTATGG
 TTATTNCCATTGGTNCCCCCANTGTTTGGGGNGTTGGCTTTGCCACCCCCCAGNGTAAA
 ACCNCCGNTGCGAATTTTTTAAACAANTTTTGGGGGTTATTANTNTTTTCCCAAAAT
 NGGCNTTTTTNCCCTTTNCCCCCCTTTNCCCNCCCNNTTCCCAACNNANCAAGGGGCC
 CCCCGGGTANTGGGGGAATAGNTTCCCCCCTTNCCCTNGNNGGGCCAATTGTGGGG
 NNNCTCCATTTGGNNTGCAAANTTCCCCCACCCNTNATTGTTGGTGGNGAAACCATTTT
 CCGGGGGGTTTGGGGGTTTTTTTTTGGTCCCNNTGCCCAANTAATTTTTGCNTTGAANA
 AAAAGAATGGGGTTTTCCAAAGCTTTTNGTCNCCATTGNTCCCTTTANGGNCCNTTN
 GTTCNCCTTNCCANAANGGGCCAATGTGAAACNNCCTTTCATTTTTTTTTATTGGGGNT
 TNCCNTTATGGN

R f 6.1

Sequence of BAC8 using primer C3S7, which spans nucleotides 1513-1532 of the cDNA. Exon sequence is underlined and represents nucleotides 1535-1588.

TTCTTGGGAGCATAGGTGCCAGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCG
 GTACGTACACAATAGCTTCTCCTCCTGGTGAGAATTTCTTCAATTTCCCTTGAGTTGTAT
 ATTGTAATGATCATTGTTGCTAGTCTTCAATGTCAATCCTATGCTTTTTTAAAAAGTGTTT
 TAAGTGTAAGTGTGAATTAACCTGAATAATCATTCTCTGCAGTAATAAAAGTTAGAAT

TCTGATTTAGGTGAGTCAGCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTC
TAGAAAACGTTCTCTAGAAAGTCCTATCTAGAAAACCTTTCTCTAGAAAGTCCTTATGTG
ATTAATAGCATCCATCCTCCCTTTTTAAATAGACTTTATTTTTGTAGAGCAGTTTTAAGT
TCACAGCAAAAGTGAGCAAAGGTACAGAGATTTCCCATATACCCCTTAGTATGCGTAG
CCTCCCCCATTATTAACATCCCCCATCAAGAGTAGTGCATTTGTTGTAAGTGGTGAACC
TACATTAACACATCATCACCCAGAGTCCGCAGTTTACATTAGGGATCATTCATATAACA
TCTATTTTTACTTTTTTTTTTTTTAGTTGAGACAAGATTCTCGCTCTGTCACCCAAGCTGG
AGTGCAGTCCGNGTGGATTGTNGGCTTACTGNCN

Ref 6.2

Sequence of BAC9 using primer C3S7, which spans nucleotides 1513-1532 of the cDNA. Exon sequence is underlined and represents nucleotides 1547-1588.

GTGCCGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCGGTACGTACACAATAGC
TTCTCCTCCTGGTGAGAATTTCTTCAATTTCTTGAGTTGTATATTGTAATGATCATTGT
TGCTAGTCTTCAATGTCAATCCTATGCTTTTTAAAAAGTGTTTTAAGTGTAAGTGNAA
TTAACTTGAATAATCATTTCTCTGCAGTAATAAAAGTTAGAATTCTGATTTAGGTGAGT
CAGCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTCTAGAAAACGTTCTCTA
GAAAGTCCTCTCTAGAAAACCTTTCTCTAGAAAGTCCTTATGTGATTAATAGCATCCATC
CTCCCTTTTTAAATAAGACTTTATTTTTGTAGAGCAGTTTTAAGTTCACAGCAAAAGTG
TAGCAAAGGGCAGAGATTTCCCATATACCCCTTAGTATGCGTAGCCTCCCCCATTATTA
CATCCCCATCAGAGTAAGNGCATTTGTTGTAAGTGGNGAACCTACAATTNACACATTN
TNACCCACAGTCCCGCAGGTTTACATTTATGGGATCATTCCCCTANTAACACCTATTT
TTTTACTTTTTTTTTTTTTTTAGGTTGAGACAAGAATTTTCGGCTTCTTGTGTACCCCCAA
ACTNGGTAGTAGNCNNACCGTCGNGNAATTTNTGGGGTTTCNTNGNGNNCANTTTGTG
CNNTCNNCTTNNCNCCNAAAGAANTTTTTTTTACCCTTTTTTTCCCCCNAANANANN
ANCCTTCCCCTTGGNGGANGCTGGGGACTTCCNCAGNGGNGG

Ref 7.1

Sequence of BAC8 using primer C3S8, which spans nucleotides 1842-1860 of the cDNA. Exon sequence is underlined and represents nucleotides 1861-1917.

CAAAGTGCAGTTTATCTCAAACTGTTTTGCTCACAGAGAGCCTTGGTTTCAAAGGTAG
GTTATTTTGTACCTGCAGTGTTGTCAGACTTTGTTTTTTTTTATTAACATTGTCTAAGATC
ATTTGACACATTCAATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAA
AATTTAAATAATAACCTAAGACCCTTAATTCTTCTTGCCTCTCTACTGCTGCCTGCCTT
TTAGAATTTTTCATTTATTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAAC
TTGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTG
TTTTCTCTTCACTTGGTTCTGTTTTTATAAAAACTCAATTTATAAAGAATTCAATATAT
AAGCAATTCAACCCACTGAAATTATTTTATGATGAATGGAAAAGAAGGTATGTGTTTG
TTCAACTGCTTTAAATGTTTACTTCTTATATTTGTTTTCCCTTAGAAATATGTATATTCTT

AAATTTTGAAGGTAGCTATTTCAATTTAATCATCCTAGAGGATGGAATGCANAGATGTT
GGATGAAAATAACTTACGTATTATTTTGTAATAAATAAGAATTCATATATGGTTGAT
TACCTAAGTGGTTTTATGCACATTCTGATAGAAAGCTTCACCAACAATCCCTTGNTNGA
TATATTATTT

Ref 7.2

Sequence of BAC9 using primer C3S8, which spans nucleotides 1842-1860 of the cDNA. Exon sequence is underlined and represents nucleotides 1864-1917.

AAGTCAGTTTATCTACAACACTGTTTTGCTACACAGAGAGCCTTGGTTTCAAAGGTAGG
TTATTTTGTACCTGCAGTGTGTCAGACTTTGTTTTTTTTTATTAACATTGTCTAAGATCA
TTTGACACATTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAAA
ATTTAAATAATAACCTAAGACCCTTAATTCTTCTTTGCCTCTCTACTGCTGCCTGCCTTT
TAGAATTTTTTCATTTATTTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAACT
TGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTGN
TTTCTCTTCACTTGGTTCTGTTTTTATAAAAACTCAATTTATAAAGAATTCAATATATA
AGCCATTCACCCACTGAAATTATTTTATGATGAATGGAAAAGAAAGGTATGTGTTTGT
CACCTGCTTTAAAATGNGACNTCNTAATATTTTGGNTTCCCCTTAAGAAAATATGTAT
AATCCTTAAAANTTTNGAAAGGGANGCTANTTTTCATTTTTTNAATCAATCCTAANAGG
GATTGGGAAATGCNCAAGATTTTTTGATTGAAAAANAACCTTANCGNATTTAATTTTTN
GGNAATAAAAATAATTAGNAATTCCNTATTATGNTTNGAATTACCTAAAGTGGTTTTTAT
TGCCCCATTTCTNTTGATATGNAAAGCCTTTCACCAACCAAATTTCCCNNTTGNNAGGAAT
ATTATTTTTTNANGGGCCTCNTNTTGTGGGGNTGGAAGNAAAAACCTTTGTTCCAAAG
GGTCCCCNC

Ref 8.1

Sequence of BAC8 using primer C3S10, which spans nucleotides 2412-2431 of the cDNA. Exon sequence is underlined and represents nucleotides 2432-2523.

AGTGCTAGTCCTCAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAA
ATATCTTCCTGTGGGATGTGTAACATTTTCAGGTAGGAATCTTCAGATGTACATTAAAT
CAAGGTATATCTTTTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTAGTTTAT
AAGGAAAGCTTAAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTTACAGTG
ATTGTCATTAATAACATTTTTAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTTA
CCTCTGAATTATCAGCACTATGCTTATTTATTCTCTTTGGCTTTACTGNCTTGNAATCCC
GTTACATACTTTAACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATT
CTTAATTGGCTTTTACTTCACATAGCAGATATACCAACATTCTCTATTCCCTACATAAA
ATATTAAGATTATTTTATGACTAATACCCATGACTCACAGATGAGTTTGCCCTCTAGTA
GGGTCATAATTCTGACCCACTAGTTGAATTCTCTGCTTACCAAGAGNCAGGTATGCTTG
CTTTTTCTTCAAACCTGTAAATAGTAGGNTTGGGGATATTNTAAAAATTAGGTAAAT
GGTATATCTTCTGGTGGAAANCAGAAAN

Ref 8.2

Sequence of BAC9 using primer C3S10, which spans nucleotides 2412-2431 of the cDNA. Exon sequence is underlined and represents nucleotides 2444-2523.

CAGCAGCACTTGTGCTGAATATTTGAGCATGCTGGAGGACCGGAAATATCTTCCTGT
GGGATGTGTAACATTTTCAGGTAGGAATCTTCCAGATGTACATTAAATCAAGGTATATC
TTTTTTTGGTTTTAGCTTTTCTCACTGGTGTGTTAGATTTTTTTAGTTTATAAGGAAAGCTT
AAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTTCACAGTGATTGTCATTAA
TACATTTTTTAAGGAGTACTTCTTGTTGATTCTCTTCCACAGTTTCTTACCTCTGAATTA
TCAGCACTATGCTTATTTATTCTCTTTGTCTTTACTGCCTTGTAATCCGTTACATACTTT
AACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATTCTTAATTGGCTT
NTTACTTCACATAGCAGATNTACCAACATTCTCTATTCCCTACATAAAAATATTAGGATT
ATTTTATGACTAATAACCATGACTCACAGATTGAGTTTGCCCTCTANTAGGGTNCATAAT
TTCTGACCCACTAGTTGAATTCTCTGCTTACCAAAAAGTCANTTATGCCTTTGCTTTTTCT
TCAAAACCCTGNTTAATTAGGNACGGCTTTGGAGATAATTTATAAAAAATTTCAAGCT
NAAANTGGNTTATTATTCNTTCCNNGGTTGAAAAAACCCAGGAATTGGCACAAANNAA
NAAAAAGNTTATTCCNNGGTTTCTTTNCGGNAAAAAACCAAAAAATCTTNGAAATTGT
TTTTTACCAAAAANGACCTCCNCGGGGAAAAAGGGNGTAAATTTNTTCCNTAAAAACN

Ref 9.1

Sequence of BAC9 using primer C3S11, which spans nucleotides 2679-2698 of the cDNA. Exon sequence is underlined and represents nucleotides 2711-2799.

TTCCTATTCATGAAGCTAATCGGGATGCAAAGAACTATCCACAATTCATGGTAAACT
TCAAGAAGCATTTCAGCAAAATTGTTTCATCAGGTAATGATTCCAATTTCTAGCTTCACTA
TAAAGGGAAAAAACTGTCTGAAAGCATTAAATGTTGTTTTGCACTGATGTCAAACCTAGA
TCCCGTGAAATGACCATTTTAATCAGACTACAAATGAGCGGTCAAATGATAGTTTCAT
GGCCAAAGCAAAGCTCATTAACAATAAAAATGAATTCACCTAAAGTAAATGGTGATCA
TCATAAACTTTCTGCATAGCTTTTTTTTTTTTCATTTTTGAATTATTAATTAAGCAAGTTTT
TAAAAATTGTGATTTTCTGTTTCACAAGGNAAGATCATAAGTTGNGGAATCTCATTTTT
AAAAATTGATACCCTATTNCTTTTGCTGNGGAAAAANTGGAAGTTTTTTAATATTTTCAA
GGTTTTTTTTTAAATTNAAATGGATTGTGGAAAACCTTTTAAATNAATTTAAACCTAC
CTAAATANTTTTTTTAATGGNCCNNGCCANCTGGAACCNTTTTATTTTTTTCCCCTAG
GAATGGTTTTACCCAAATCCATTCCCTTTTGAATAATTTTTTCCCTNAATTNCCCAA
AAANTTTTTNTTTTTTTGGGNGGAAAAAATANTTGGAAAATTAAAAAAATGGGGGTGG
GGCNTAAATGGGGATTATTTTTAAATTTCTAAAAAAGGGANTTTTCCATTTACCTTT
NAATCCTTTTTGGGNGGN TTCNATTTATTGGGGAATCCTNCNCTTTTTNTNCNCCTTA
AAAAANTTAGGGCCTNCCAAAATTTTAAACCNTTTAATTTTTNAAAANGGAAAGGGNC
CCCTTTCTTNGCCCGGTTGTTT

Ref 10.1

Sequence of BAC8 using primer C3S12, which spans nucleotides 2908-2927 of the cDNA. Exon sequence is underlined and represents nucleotides 2928-2941.

TACAGATTGGAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCT
CTCTGATGATTAGACTTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAA
ATAAACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAAT
CTTTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTGGAGACTATTTTACACAT
ATTTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTA
TAATCCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTGAACTA
GAACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACCTGGTT
CCAGGTGAGGTTTCTTTAGAACGTAAAAGCCTGAAATCACACCTTAAAAACACTTCCT
TTAACCTTTATAATTTCTTAATTTTACCATAAATGATTGCGTTTTATATTTACTGGGGC
TAAGTAGNATTTCTGNTATAGGTATTCTTTCCAACCTTTCTCTATTTTTTGTACTCAA
AGTGTAGTGGATGGACCGGAAGCATTGGGGTTCACCTGGGAGAATGGTTGGNAATGC
AGAACCCTTAGACCCCAACCCAGCCCCTGTGAAA

Ref 10.2

Sequence of BAC9 using primer C3S12, which spans nucleotides 2908-2927 of the cDNA. Exon sequence is underlined and represents nucleotides 2930-2941.

CAGATAGTAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCTCT
CTGATGATTAGACTTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAAAT
AACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAATCT
TTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTGGAGACTATTTTACACATAT
TTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTATA
ATCCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTGAACTAG
AACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACCTGGTTC
CAGGNGAGGTATCTTTAGAACGTNAAAGCCTGAAATCACACCTTAAAAACACTTNCTT
TAACCTTTTATAANTTNCTTAATTTTACCATAAAATNGATTGCNGTTTTATATTTTAC
CTNNGGNCTANACCTNAGGCAATTTTTCTGGGTCATAAGGGAAATTTCTTTTTCCCAA
CCCTTTTCTTCTTATTTTGTGTTGGGNCACTCCCAAAGGTGNTCNGTTGGGGNTTNGGG
NCCCCGNGAAAGGCCATTTGGGGGNTTACCCCCGGGGGANGATTTGGTTTTGGAAAA
TNGTCNNNAAAACCTTCCNNACCCCCNNCCCCCNGGCCCCCNCTGNNNGGAAATCCAAA
AGGATCTTGNCNATTTTTTTANCCAAANGANCNCCCCCNAGGGNNGGATTTTNGTTAT
TTCCCAANAAGANGTAAGGTTNTTGGCCTTTNGGGGCNTTGGGTGTTTTNTTTNN

Ref 11.1

Bac 9 sequenced with HC3AS3, which spans nucleotides 3376-3393 of the cDNA. Exon sequence is underlined and represents nucleotides 3267-3289.

CTGANGTGTNGCAANGCCACTCCTGTGTCTTTTCTGCATGTCCTCAATAGCAACTTCAA
TCCGTGTAAAGATGATCTGAGTNANNGAGCATCTGTTANATCAGNGTACTGACTGAAA
CTATTTAATGAACTTTATGTATAATCAACTGAAATTAGANAAAAAAGATCAATNGT
AACTTCATGTAAACAATAAAATTCCAACTTGGATTCTAAATGAANNAAAAANATCAA
CCTTTAAAGAAAAGCTGGGGGTGAATAAGGGCTTAGAAAAGANGTANAAAATGANGA
CTCAAAATGGTAAAGGGTCTAATATGNATGGATAAGGATGGACATATCTTCGGACTCT
GAGTGGTGTACATGGCTTGATGATTGCTCACTATGTGTGNCATTATGGCTACCTCTCTT
TAGGCATGCCTGTTAANTAGGAAGCTGAACTANCAAAGNCTCTTNGATGTATNANTCC
TGCCGCTNAAAGAAGGGGNCGCNTGANNCAAATGATTTGCNATGTNTCTGCTATNATNG
NAAGNGNTCCTNGANTNNTTCNGANAAANCTCTCNANGAGNCTAGTTTACATNCGGTC
AGNGCTTCTTGCACTCCTGNGCATCTCCCGTANTTCACCTCATTNNACCNTNANTTT
ATAANNANNNAGCCCACTNNCCTATAGGCNATCNACGCNNTTCCCNNTANTCANTNN
NAGACAATTTTTTNNCGCCCCCTCCTNNTCCTTCCTNNCTTCNCCCNNCNCNCCCTNTN
TCNTNCCCCCNCCNNTTCTTANCTTCT

Ref 12.1

Sequence of BAC9 using primer C3S15, which spans nucleotides 3750-3769 of the cDNA. Exon
 sequence is underlined and represents nucleotides 3779-4118, and also represent the 3' terminus of
 the transcriptional unit.

TGTGAAAAGATCTATTGGAAAACAACATGGAATGGAATTCTGGAAATTATTATTNATT
GAAGAATGCAGTGGCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATG
GCTATGGTTTCTAATGTTCTGGTAACAAGCTGTTATCTTTTAAGACATTTTAATGACTC
AAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTAAAAATTTATTCA
CTTTAAGTTCGTATTTTTTAATTTATATTACCATTATATAGATTCATTTTGGAACCATTTT
AAATGTAGTAATGCTTATTTTAAAGGTACTATTAATATGTGAATGTTTACACTAATTT
TACCGAGTGGGACTTCAAAATTTTATTATTGACAATGGCTGAGAACAAATTNAAGGGT
TTGACTCNAGAACTANTTCCAAACCTAGCAGAATAAAAATCATAGATAGCCCCAAATT
AATGAGTTTGGGNAACTGTNTCAAAGTTTTTTTCCATTACATACCCAAAAACAGGAA
ATTTTAGAATTTGCCNGAACCTTTACCTTAAGANAAAAACCCTTTTGTGNTNAAAAATN
TANTNTTAAAATTCCCGGGGGGANTAATCTTAATNACCCCGGGTGGGGCCANNCNCCC
CNTTATAACTTTGGAATTTAAAAATTCNTTTTTNTNCAACCCCAAACCTGNANTNGGGT
NNTTTTNAAGGAAAACCTTCCACTNGGAAGTTNNCTTTTAGGGNCCNANCCTNCNAN
AAANNGGGGAANATTGGGAAGTCTTCCCCTTCNTTNGGGGGGNGNCCCCAAAAAATTCT
TAATAAANCCCCGGGGCTCCCATNTTGNATTTTTTTTTTTGGCCCCACACTGTGTT
NATTAAANCCCCNCNTGCTAAAAATTTTTNNNGAAAAANACCTNAACCCTTCTNNA

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPFFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPFFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----

HC2A	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T Y T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T Y T I L K P S A D F L T S N
 rat -----
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G --- S V R --- E
 HC5 -----

Cadherin
Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat -----
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A R K S R F E P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5 -----

1.1/1.2/2.1/2.2

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D E K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L
 rat -----
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N --- D Y I S --- G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K C F T F M D R G C V F K M V N --- N Y I S --- M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y Q V S S K L Y S L P N P S V I V S L R L D F L
 HC5 -----

3.1/3.2

HC2A R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 rat -----
 HC4 Q T I C N H E H Y I P L N L P M --- A F A K F K L Q R --- V Q D S N L --- E Y S L S E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D L T P S E S --- T Q E L H A S D M P E Y S V T N E F
 HC3 R I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S --- V P F
 HC5 ----- M N A D T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

4.1/4.2

Cadherin
EC motif

HC2A C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S H S H Q A R I A T
 KIAA C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat -----
 HC4 C K H H F L V G L L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D --- V R H L A L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S
 HC3 R Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G I L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat -----
 HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A M P N S A S R D E F P C G --- F T S P --- A N --- R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- G A I T

5.1/5.2

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HC2A      LQVVISVSQLIADVVVGIGETRFOQSLSIINNCANSDRLIKHTSFSSDVKD LTKRIRTVLM
KIAA      LQVVISVSQLIADVVVGIGGTRFOQSLSIINNCANSDRLIKHTSFSSDVKD LTKRIRTVLM
rat       LQVVISLSQLIADVVVGIGGTRFOQSLSIINNCANSDRLIKHTSFSSDVKD LTKRIRTVLM
HC4       LQIIIAVSQLIADVALSGGSRFOESLFIINNFANSDRPLARAFPAEVKD LTKRIRTVLM
HC1       LQLIKAVSLIAD-AGIGGSRFQHS LAITN NFANGDKOMQNFPAEVKD LTKRIRTVLM
HC3       MQVPMSSLSVLGAD-AGIGGSRFQHS LAITN NFANGDKOMQNFPAEVKD LTKRIRTVLM
HC5       MQVPMSSLSVLGAD-AGIGGSRFQHS LAITN NFANGDKOMQNFPAEVKD LTKRIRTVLM

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FIG. 4
3 of 5

Refs

		Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLFSEAAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLE	SMARIHARNGDLSEAAAMCYIHI
HC3	DTVQMKHEHQEDPEMLIDLMYRIAKGYQTS	PDLRLTWLQNMAGKHSERSNHAEEAAQCLVHS
HC5	DTVQMKREFOEDPEMLMDLMYRIAKSYQAS	PDLRLTWLQNMAEKHTKKKCYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYLIRKGV		FRQGCTAFRVIITPN
KIAA	TALVAEYLIRKEA	VQWEPPLPHSHSACLRR	SRGGVFRQGCTAFRVIITPN
rat	TALVAEYLIRKEAD	LALQREPPVFPYSHTSCQK	SRGGMFRQGCTAFRVIITPN
HC4	AALVAEFLIRKKL		FPNGCSAFKKIITPN
HC1	AALIAEYLIRKGYWKVEKICTASLLSE	THPCDSNSLLTTPSGGSMFSGMGP	PAFLSITPN
HC3	AALVAEYLSMLED		RKYLPGVCVTFCNISSN
HC5	AALVAEYLSMLED		HSYLPVGSVSFQNISSN

8.1/8.2

		ITAM
HC2A	IDEEASMMEDVGMQD	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP
KIAA	IDEEASMMEDVGMQD	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP
rat	IDEEASMMEDVGMQD	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD	VHYSEEVLLLELLEQCVNGLWKAERYEISEISKLI GPI
HC1	IKEEGAAKEDSGMHD	TPYNNILVEQLYMCGEFLWKSEYELIADVNKPIIAV
HC3	VLEESAVSDDVVS	PDEEGICSGKYFTESGLVGLLEQAAASF
HC5	VLEESVVS	EDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLIIP

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD			
KIAA	YEKRRD	FERLAHLN	YDTIHRAYSKVTEVMHSGRLLGT	YFRVAFFGQAQYQFTDSETDVE
rat	SMKSGGT	LETTHLYD	TIHRFYSKVTEVITR	AAGSWDLLPGGLFGQ
HC4	YENRRE	FENLTQVYRT	IHGAYTKILEVMHTKKRLLG	TFFRVAFYGQ
HC1	FEKQD	FKKLS	SDLYYD	JHRSYLVKVAEVVNSEKRLFG
HC3	HEANRDA	KQLSTI	HGKLOEAF	SKIVHQS
HC5	LEAHRE	FRKLT	LTTHSKLQRA	FD

9.1

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTP	PLSEISQRLKLIYSDRFGSENVKMIQDSGKVNPKDLDSHYA
KIAA	GFFEDEDGKEYIYKEPKLTP	PLSEISQRLKLIYSDRFGSENVKMIQDSGKVNPKDLDSHYA
rat	GFFEDEDGKEYIYKEPKLTP	PLSEISQRLKLIYSDRFGSENVKMIQDSGKVNPKDLDSHYA
HC4	SFFEEDGKEYIYKEPKL	TGLSEISLRLVKIYGEF
HC1	GFFEEDGKEYIYKEPKL	TGLSEISQRLKLIYAD
HC3	TKFGDL	DEQEFVYKEPAITKLAEIS
HC5	SKFGDL	DEQEFVYKEPAITKLPEIS

10.1/10.2

	ITAM
HC2A	YIQVTHVIPFFDEKELQERKTE
KIAA	YIQVTHVIPFFDEKELQERKTE
rat	YIQVTHVIPFFDEKELQERKTE
HC4	YIQVTHVIPFFDEKELQERKTE
HC1	YIQVTHVIPFFDEKELQERKTE
HC3	YIQVTHVIPFFDEKELQERKTE
HC5	YIQVTHVIPFFDEKELQERKTE

B

Coiled-Coil 1

HC2A	IHCFFYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLQSSV
KIAA	IHCFFYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLQSSV
rat	IHCFFYVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELHQLCSSAEVDMIKLQKLQSSV
HC4	SNSFFYVKKRIPINCEQQINLKH	IDGATDEIKDKTAELOKLCSSSTDVDMIQLOKLQSSV
HC1	SHLFFYVKKRIQVISOSSTELNFI	IEVAIDEMSRKVSELNQLCTMEEVDMISLOKLQSSV
HC3	SHAFPIKTRVNVTHKEFI	ILTHIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLOQSV
HC5	MHAFPIKTRISVIQKEEFVLTH	IEVAIEDMKKKTLQLAVAINQEPDAPKMLQMVLOQSV

11.1

Coiled-Coil 2

HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKTMFRKFIQACSILLELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

Coiled-Coil 2

HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMYTS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----
rat	YQEEMKANYREIRKELSDIIVH	RICPGEDKRATKFFPAHLQRHQRTDNKHSGSRVDQFELS
HC4	YHEGLKSNFRDMVKELSDIIEH	QILOEDTMHSPWMSNTLHVFCASISGTSSTRGYGSPRYA
HC1	YQEELRSHYKMLSELSTVMNE	QITGRDDLKSK---RGVDQCTRVISKATPALPTVSIS
HC3	YQRELG---	KLSS-----PZ-----
HC5	YQQLKKNYNKLKENLRPMIER	KIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQSSC-

PBM

HC2A	SSVVZ-----
KIAA	-----
rat	CVTLPHPEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVI FNSRFYRSWGK
HC4	EVZ-----
HC1	SAEVZ-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

FIG. 5

1/1	ATG GCC GAG CGC CGC GCC TTC GCC CAG AAG	31/11	ATC AGC AGA ACG GTG GCA GCC GAA GTT AGG
Met ala glu arg arg ala phe ala gln lys	61/21	91/31	ile ser arg thr val ala ala glu val arg
AAG CAG ATC TCC GGA CAA TAT AGT GGT TCT	121/41	151/51	pro gln leu leu lys asn leu asn ile val
lys gln ile ser gly gln tyr ser gly ser	181/61	211/71	leu thr glu ala val asp pro val asp leu
GGC AAT ATA TCC CAT CAC ACC ACA GTG CCC	241/81	271/91	glu asp tyr leu ile thr his pro leu ala
gly asn ile ser his his thr thr val pro	GAA TTT CCT CCA GAT GAT ATT GAA GTT GTT	331/111	val asp ser gly pro leu arg asp leu ile
GAA GAT TAC CTC ATT ACT CAT CCT TTG GCT	361/121	391/131	TAT AGT CCT CGG GAC TGC AGA ACT CTT GTT
glu asp tyr leu ile thr his pro leu ala	ACA GAA GAC TGG GCA ATT GTC ATC AGA AAA	451/151	tyr ser pro arg asp cys arg thr leu val
241/81	thr glu asp trp ala ile val ile arg lys	511/171	tyr his lys leu gly thr gly phe asn pro
GAA TTT CCT CCA GAT GAT ATT GAA GTT GTT	421/141	571/191	AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA
glu phe pro pro asp asp ile glu val val	AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA	631/211	AAA GGT TTG CCA AAA CAA GTT TTT GAA TCT
301/101	asn thr leu asp lys gln lys glu arg gln	691/231	lys gly leu pro lys gln val phe glu ser
TCA GCT GTA CCT GAA GAA AGT GAA ATG GAT	GAT GAA GCT CCA GAT GGC AAC AGC TAC CAG	751/251	AAA GGT TTG CCA AAA CAA GTT TTT GAA TCT
ser ala val pro glu glu ser glu met asp	asp glu ala pro asp gly asn ser tyr gln	811/271	lys gly leu pro lys gln val phe glu ser
361/121	541/181	871/291	leu ser val pro asp ile pro lys glu his
ACA GAA GAC TGG GCA ATT GTC ATC AGA AAA	ATG TCA ATA GAT GAT ACC CCA AGG GGT AGC	931/311	CTT AGT GTT CCT GAT ATA CCC AAA GAA CAT
thr glu asp trp ala ile val ile arg lys	met ser ile asp asp thr pro arg gly ser	991/331	leu ser val pro asp ile pro lys glu his
421/141	601/201		
AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA	TCA CTT CCT GAT GCT TTG CTT CCC AAT TTA		
asn thr leu asp lys gln lys glu arg gln	ser leu pro asp ala leu leu pro asn leu		
481/161	661/221		
GAT GAA GCT CCA GAT GGC AAC AGC TAC CAG	CGT CAG AAT GAT GAC CAA AGG AAA TCA AAC		
asp glu ala pro asp gly asn ser tyr gln	arg gln asn asp asp gln arg lys ser asn		
541/181	721/241		
ATG TCA ATA GAT GAT ACC CCA AGG GGT AGC	TCA CCA GAT GAG GAA GAA CCA ATA GAA CGG		
met ser ile asp asp thr pro arg gly ser	ser pro asp glu glu glu pro ile glu arg		
601/201	781/261		
TCA CTT CCT GAT GCT TTG CTT CCC AAT TTA	TTT GGT CAA AGA CTT CTT GTA AAA TGC TTA		
ser leu pro asp ala leu leu pro asn leu	phe gly gln arg leu leu val lys cys leu		
661/221	841/281		
CGT CAG AAT GAT GAC CAA AGG AAA TCA AAC	ATT TTT GCA AGT TTG GCT TTA TAT GAT GTC		
arg gln asn asp asp gln arg lys ser asn	ile phe ala ser leu ala leu tyr asp val		
721/241	901/301		
TCA CCA GAT GAG GAA GAA CCA ATA GAA CGG	TAT TTT GAC CTT AAT TCT GAG CAG ATG AAA		
ser pro asp glu glu glu pro ile glu arg	tyr phe asp leu asn ser glu gln met lys		
781/261	961/321		
TTT GGT CAA AGA CTT CTT GTA AAA TGC TTA	GCC ATT ACT ACC CTG GCA AGA TCA GCA ATT		
phe gly gln arg leu leu val lys cys leu	ala ile thr thr leu ala arg ser ala ile		
841/281			
ATT TTT GCA AGT TTG GCT TTA TAT GAT GTC			
ile phe ala ser leu ala leu tyr asp val			
901/301			
TAT TTT GAC CTT AAT TCT GAG CAG ATG AAA			
tyr phe asp leu asn ser glu gln met lys			
961/321			
GCC ATT ACT ACC CTG GCA AGA TCA GCA ATT			
ala ile thr thr leu ala arg ser ala ile			

1021/341
 TTT CTT GTA ATA AAG CTA GAA AAA GTC CTA
 phe leu val ile lys leu glu lys val leu
 1081/361
 CCA TAT ATG ATT TTC AAA GAA GCA GAT GCC
 pro tyr met ile phe lys glu ala asp ala
 1141/381
 AAG AGT CAA GCA GAT CAG TTT TGC CAA AGA
 lys ser gln ala asp gln phe cys gln arg
 1201/401
 ACT GCA ATC CAT TTA ATG AAT ATT GTT AGC
 thr ala ile his leu met asn ile val ser
 1261/421
 GAA GTA GAA ATC AGT ACT GGA GAA CGA AAA
 glu val glu ile ser thr gly glu arg lys
 1321/441
 ATT GTT GGC AGA CGA TCA CTT GAA AGG ACA
 ile val gly arg arg ser leu glu arg thr
 1381/461
 AGC TTT CGA CCA GCT ACT CTC ACA GTG ACA
 ser phe arg pro ala thr leu thr val thr
 1441/481
 AGT GAT GAA GAT CTC TAC AAA TTC CTT GCT
 ser asp glu asp leu tyr lys phe leu ala
 1501/501
 CGA CTA AGA CCT ATT ACA GCT CAG CTC AAG
 arg leu arg pro ile thr ala gln leu lys
 1561/521
 CAT TAT TGC CTA ACT CCG GAG CTG CTT CAA
 his tyr cys leu thr pro glu leu leu gln
 1621/541
 CCT ACC AGA GAA ATC TTA GAG TTT CCC GCA
 pro thr arg glu ile leu glu phe pro ala
 1681/561
 AGA AAT CTT CTC TAC ATA TAC CCT CAG AGT
 arg asn leu leu tyr ile tyr pro gln ser
 1741/581
 AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG
 arg asn ile thr val lys val gln phe met
 1801/601
 GTA ATC TTT GGT AAA TCT AGC TGT TCA GAA
 val ile phe gly lys ser ser cys ser glu
 1861/621
 TAT CAT AAC AGG TCT CCT GAT TTT CAT GAA
 tyr his asn arg ser pro asp phe his glu
 1921/641
 ACT GAC CAT CAT CAC TTG CTT TTT ACT TTT
 thr asp his his his leu leu phe thr phe
 1981/661
 ACT CCT CTT GAA ACA CCA GTT GGA TAT ACA
 thr pro leu glu thr pro val gly tyr thr
 2041/681
 AAG ACT GGC CAG TTT TGC TTG CCA GTC TCA
 lys thr gly gln phe cys leu pro val ser
 2101/701
 CTG TCT CCT GAG GTT CCT CTA CCT GGC ATG
 leu ser pro glu val pro leu pro gly met

1051/351
 CAG CAA GGA GAC ATT GGA GAG TGT GCA GAA
 gln gln gly asp ile gly glu cys ala glu
 1111/371
 ACC AAG AAT AAA GAA AAA CTG GAG AAA CTG
 thr lys asn lys glu lys leu glu lys leu
 1171/391
 CTT GGG AAA TAT CGC ATG CCT TTT GCT TGG
 leu gly lys tyr arg met pro phe ala trp
 1231/411
 AGT GCT GGG AGT TTG GAA AGA GAT TCT ACA
 ser ala gly ser leu glu arg asp ser thr
 1291/431
 GGG TCT TGG TCA GAG AGG AGG AAT TCT AGT
 gly ser trp ser glu arg arg asn ser ser
 1351/451
 ACA AGT GGA GAT GAT GCT TGT AAC TTG ACG
 thr ser gly asp asp ala cys asn leu thr
 1411/471
 AAT TTT TTT AAG CAG GAA GGA GAC CGC TTA
 asn phe phe lys gln glu gly asp arg leu
 1471/491
 GAT ATG AGA AGG CCA TCT TCT GTC TTA CGG
 asp met arg arg pro ser ser val leu arg
 1531/511
 ATA GAC ATT TCT CCC GCA CCT GAA AAT CCC
 ile asp ile ser pro ala pro glu asn pro
 1591/531
 GTG AAG CTT TAC CCT GAC AGT AGA GTT AGA
 val lys leu tyr pro asp ser arg val arg
 1651/551
 AGG GAT GTT TAT GTT CCA AAC ACT ACT TAC
 arg asp val tyr val pro asn thr thr tyr
 1711/571
 CTT AAT TTT GCC AAT CGT CAA GGT TCT GCT
 leu asn phe ala asn arg gln gly ser ala
 1771/591
 TAT GGA GAG GAT CCA AGC AAT GCC ATG CCG
 tyr gly glu asp pro ser asn ala met pro
 1831/611
 TTT TCA AAG GAA GCC TAT ACA GCC GTA GTA
 phe ser lys glu ala tyr thr ala val val
 1891/631
 GAA ATC AAG GTT AAG CTT CCT GCT ACT TTA
 glu ile lys val lys leu pro ala thr leu
 1951/651
 TAT CAT GTT AGT TGT CAA CAA AAA CAA AAT
 tyr his val ser cys gln gln lys gln asn
 2011/671
 TGG ATA CCA ATG CTT CAG AAT GGA CGG TTG
 trp ile pro met leu gln asn gly arg leu
 2071/691
 TTG GAA AAA CCA CCA CAG GCT TAT TCT GTA
 leu glu lys pro pro gln ala tyr ser val
 2131/711
 AAA TGG GTA GAT AAT CAC AAA GGT GTT TTT
 lys trp val asp asn his lys gly val phe

2161/721
AAT GTT GAA GTT GTT GCT GTT TCG TCT ATC
asn val glu val val ala val ser ser ile
2221/741
TTT GCT CTG GTC AAT GCT CTG GAT GAA CAC
phe ala leu val asn ala leu asp glu his
2281/761
ATC ATG GAA AAT AAC TTA GAA AAT GAA TTG
ile met glu asn asn leu glu asn glu leu
2341/781
CAG CTG GAA CCA GTG GTC CGA TTT CTT CAT
gln leu glu pro val val arg phe leu his
2401/801
ATT AGA CCT CCT GTC ATT GCT GGC CAA ATA
ile arg pro pro val ile ala gly gln ile
2461/821
ATG GCA TCA ATT ATA AAT CGA CTT CAC AAA
met ala ser ile ile asn arg leu his lys
2521/841
AGA AAC AGC CTT CTT GCA TCA TAT ATT CAT
arg asn ser leu leu ala ser tyr ile his
2581/861
AAT TCA TCA TCA CCA GGT CCT GGG GGT TTG
asn ser ser ser pro gly pro gly gly leu
2641/881
AGA TCT GCG GTG AGA CCT GCA AGC CTT AAT
arg ser ala val arg pro ala ser leu asn
2701/901
AAT CCA GAT ATA TCT GGG ACT CCC ACG TCA
asn pro asp ile ser gly thr pro thr ser
2761/921
AGT AAG GGT TTA GAT CGC TCC AAT TCC TGG
ser lys gly leu asp arg ser asn ser trp
2821/941
TGG GGA TCC AAC CCC AGT CCA AGT GCA GAA
trp gly ser asn pro ser pro ser ala glu
2881/961
CGT ATG TCT TCG CAC ACA GAG ACG TCA AGT
arg met ser ser his thr glu thr ser ser
2941/981
ACT AAA AAG CTT TTT CAC GAG GAG CTG GCT
thr lys lys leu phe his glu glu leu ala
3001/1001
CGG GAA TCA GCT TTG CAA CAA GCC TGG TTC
arg glu ser ala leu gln gln ala trp phe
3061/1021
CAC CAT TTA TAC TTT AAT GAT AAA CTT GAG
his his leu tyr phe asn asp lys leu glu
3121/1041
TTC ATG GAT GAC ATT GCA GCT CTT GTC AGC
phe met asp asp ile ala ala leu val ser
3181/1061
CAG AAG GAC ACA GAA ATG GTT GAG AGA CTC
gln lys asp thr glu met val glu arg leu
3241/1081
CTG TTG TCT GTT ATG GAC AGA GGA TTT GTT
leu leu ser val met asp arg gly phe val

2191/731
CAT ACA CAA GAT CCT TAT CTT GAC AAA TTT
his thr gln asp pro tyr leu asp lys phe
2251/751
CTG TTC CCA GTC CGA ATT GGG GAC ATG CGA
leu phe pro val arg ile gly asp met arg
2311/771
AAG AGC AGT ATT TCA GCA CTG AAT TCA TCC
lys ser ser ile ser ala leu asn ser ser
2371/791
CTT CTG CTA GAT AAA CTG ATA CTT TTA GTT
leu leu leu asp lys leu ile leu leu val
2431/811
GTT AAC CTA GGT CAA GCA TCT TTT GAA GCC
val asn leu gly gln ala ser phe glu ala
2491/831
AAC TTG GAA GGA AAT CAT GAC CAG CAT GGC
asn leu glu gly asn his asp gln his gly
2551/851
TAT GTT TTC CGC CTA CCA AAT ACT TAC CCT
tyr val phe arg leu pro asn thr tyr pro
2611/871
GGA GGA TCA GTG CAT TAT GCC ACA ATG GCT
gly gly ser val his tyr ala thr met ala
2671/891
TTA AAT CGT TCT CGA AGC CTT AGT AAT AGC
leu asn arg ser arg ser leu ser asn ser
2731/911
CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG
pro asp asp glu val arg ser ile ile gly
2791/931
GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA
val asn thr gly gly pro lys ala ala pro
2851/951
TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT
ser thr gln ala met asp arg ser cys asn
2911/971
TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA
phe leu gln thr leu thr gly arg leu pro
2971/991
TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT
leu gln trp val val cys ser gly ser val
3031/1011
TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG
phe phe glu leu met val lys ser met val
3091/1031
GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT
ala pro arg lys ser arg phe pro glu arg
3151/1051
ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT
thr ile ala ser asp ile val ser arg phe
3211/1071
AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT
asn thr ser leu ala phe phe leu asn asp
3271/1091
TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG
phe ser leu ile lys ser cys tyr lys gln

3301/1101	GTG TCT TCA AAG CTT TAC TCA TTA CCG AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT	3331/1111
val ser ser lys leu tyr ser leu pro asn pro ser val leu val ser leu arg leu asp		
3361/1121	TTT CTA CGA ATC ATC TGC AGT CAT GAG CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA	3391/1131
phe leu arg ile ile cys ser his glu his tyr val thr leu asn leu pro cys ser leu		
3421/1141	CTT ACT CCA CCT GCA TCT CCA TCA CCT TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA	3451/1151
leu thr pro pro ala ser pro ser pro ser val ser ser ala thr ser gln ser ser gly		
3481/1161	TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC	3511/1171
phe ser thr asn val gln asp gln lys ile ala asn met phe glu leu ser val pro phe		
3541/1181	CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT	3571/1191
arg gln gln his tyr leu ala gly leu val leu thr glu leu ala val ile leu asp pro		
3601/1201	GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC	3631/1211
asp ala glu gly leu phe gly leu his lys lys val ile asn met val his asn leu leu		
3661/1221	TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG	3691/1231
ser ser his asp ser asp pro arg tyr ser asp pro gln ile lys ala arg val ala met		
3721/1241	TTG TAT CTA CCT CTG ATT GGT ATT ATC ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA	3751/1251
leu tyr leu pro leu ile gly ile ile met glu thr val pro gln leu tyr asp phe thr		
3781/1261	GAA ACT CAC AAT CAA CGA GGA AGA CCA ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG	3811/1271
glu thr his asn gln arg gly arg pro ile cys ile ala thr asp asp tyr glu ser glu		
3841/1281	AGC GGA AGT ATG ATA AGC CAG ACC GTT GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA	3871/1291
ser gly ser met ile ser gln thr val ala met ala ile ala gly thr ser val pro gln		
3901/1301	CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT	3931/1311
leu thr arg pro gly ser phe leu leu thr ser thr ser gly arg gln his thr thr phe		
3961/1321	TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT	3991/1331
ser ala glu ser ser arg ser leu leu ile cys leu leu trp val leu lys asn ala asp		
4021/1341	GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA	4051/1351
glu thr val leu gln lys trp phe thr asp leu ser val leu gln leu asn arg leu leu		
4081/1361	GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA	4111/1371
asp leu leu leu tyr leu cys val ser cys phe glu tyr lys gly lys lys val phe glu arg		
4141/1381	ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT	4171/1391
met asn ser leu thr phe lys lys ser lys asp met arg ala lys leu glu glu ala ile		
4201/1401	CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA	4231/1411
leu gly ser ile gly ala arg gln glu met val arg arg ser arg gly gln leu glu arg		
4261/1421	AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT	4291/1431
ser pro ser gly ser ala phe gly ser gln glu asn leu arg trp arg lys asp met thr		
4321/1441	CAC TGG CGT CAA AAC ACA GAG AAG CTT GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA	4351/1451
his trp arg gln asn thr glu lys leu asp lys ser arg ala glu ile glu his glu ala		
4381/1461	CTG ATT GAT GGA AAC CTG GCT ACA GAA GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT	4411/1471
leu ile asp gly asn leu ala thr glu ala asn leu ile ile leu asp thr leu glu ile		

4441/1481
 GTT GTT CAG ACC GTT TCT GTA ACG GAA TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA
 val val gln thr val ser val thr glu ser lys glu ser ile leu gly gly val leu lys
 4501/1501
 GTG CTA CTA CAC AGC ATG GCC TGT AAC CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT
 val leu leu his ser met ala cys asn gln ser ala val tyr leu gln his cys phe ala
 4561/1521
 ACA CAG AGA GCC TTG GTT TCA AAG TTT CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG
 thr gln arg ala leu val ser lys phe pro glu leu leu phe glu glu glu thr glu gln
 4621/1541
 TGT GCT GAT TTA TGC CTC AGG CTT CTC CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG
 cys ala asp leu cys leu arg leu leu arg his cys ser ser ser ile gly thr ile arg
 4681/1561
 TCA CAC CCC AGT GCC TCC CTT TAC CTA CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC
 ser his pro ser ala ser leu tyr leu leu met arg gln asn phe glu ile gly asn asn
 4741/1581
 TTT GCC AGG GTT AAA ATG CAG GTA CCA ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG
 phe ala arg val lys met gln val pro met ser leu ser ser leu val gly thr ser gln
 4801/1601
 AAT TTT AAT GAA GAA TTC TTA AGA CGT TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA
 asn phe asn glu glu phe leu arg arg ser leu lys thr ile leu thr tyr ala glu glu
 4861/1621
 GAT CTG GAA TTG AGG GAA ACA ACA TTT CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC
 asp leu glu leu arg glu thr thr phe pro asp gln val gln asp leu val phe asn leu
 4921/1641
 CAT ATG ATT CTT TCT GAT ACT GTG AAA ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG
 his met ile leu ser asp thr val lys met lys glu his gln glu asp pro glu met leu
 4981/1661
 ATT GAT CTA ATG TAC AGA ATT GCC AAG GGT TAC CAG ACC TCT CCA GAG CGA TTG ACC TGG
 ile asp leu met tyr arg ile ala lys gly tyr gln thr ser pro glu arg leu thr trp
 5041/1681
 TTG CAG AAC ATG GCA GGC AAG CAC TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT
 leu gln asn met ala gly lys his ser glu arg ser asn his ala glu ala ala gln cys
 5101/1701
 CTA GTC CAC TCA GCA GCA CTT GTT GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT
 leu val his ser ala ala leu val ala glu tyr leu ser met leu glu asp arg lys tyr
 5161/1721
 CTT CCT GTG GGA TGT GTA ACA TTT CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG
 leu pro val gly cys val thr phe gln asn ile ser ser asn val leu glu glu ser ala
 5221/1741
 GTC TCA GAT GAT GTG GTA TCT CCA GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT
 val ser asp asp val val ser pro asp glu glu gly ile cys ser gly lys tyr phe thr
 5281/1761
 GAG TCA GGA CTT GTG GGA TTA CTG GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG
 glu ser gly leu val gly leu leu glu gln ala ala ala ser phe ser met ala gly met
 5341/1781
 TAT GAA GCA GTT AAT GAA GTT TAC AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT
 tyr glu ala val asn glu val tyr lys val leu ile pro ile his glu ala asn arg asp
 5401/1801
 GCA AAG AAA CTA TCC ACA ATT CAT GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT
 ala lys lys leu ser thr ile his gly lys leu gln glu ala phe ser lys ile val his
 5461/1821
 CAG AGT ACT GGC TGG GAG CGG ATG TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC
 gln ser thr gly trp glu arg met phe gly thr tyr phe arg val gly phe tyr gly thr
 5521/1841
 AAG TTC GGG GAT TTG GAT GAA CAA GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT
 lys phe gly asp leu asp glu gln glu phe val tyr lys glu pro ala ile thr lys leu

5611/1871

TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT
tyr gly glu arg phe gly glu asp val val.

5671/1891

AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT
lys cys lys leu asp pro asn lys ala tyr

5731/1911

GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC
asp thr tyr glu met lys asp arg ile thr

5791/1931

TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT
phe met tyr cys thr pro phe thr leu asp

5851/1951

TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT
phe lys arg lys thr ile leu thr thr ser

5911/1971

AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA
asn val thr his lys glu glu ile ile leu

5971/1991

CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA
gln lys lys thr gln glu leu ala phe ala
6221/6221

6031/2011
CMB 216 1

CCT CAG ATG GAA CTC CAG GGA TCT GAA GGC
leu gln met val leu gln gly ser val gly
6001/2031

6091/2031
CCC CAC C

GCC CAG GAT TTT CAG TCT GAA ATA CCG AGT
ala gln val phe leu ser glu ile pro ser
6151/2051

CTG CEA C

leu arg leu cys phe lys asp phe thr lys
6211/2071

AGC TTA A

ser leu ile gly pro val gln lys glu tyr
6271/2091

TAA

OCH

TATCCAAGCCAGTATTGCTTGTCCCCTGCCACAGAGATTCC
GAATGCACTTGTTTTATTTCATCTGCAAAGAGCCATGTATTC
AATGGAATTCTGGAAATTATTATTTCATTGAAGAATGCAGTG
ATCATGGCTATGGTTTCTAATGTTCCGGTAACAAGCTGTTA
ATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTAT
TAGATTTCATTTTGGACCCATTTTAAATGTAGTAATGCTTA
GCGCGCCAGGGCCTC

A. Allelic Variations: single nucleotide changes (polymorphisms) between hCLASP-3 cDNAs and/or genomic sequences

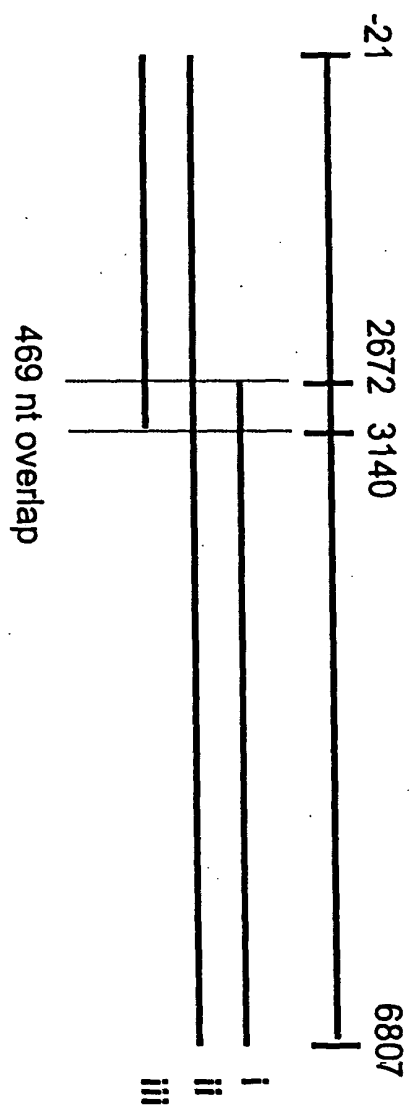
Isoform	Difference	Nucleotide position	Consequence
1	polymorphism	318	A to G; missense
2	polymorphism	323	A to G; Glu to Gly
3	polymorphism	2187	T to C; missense
4	polymorphism	3165	T to G; Asp to Glu

B. Alternative Exon usage

Isoform	Difference	Nucleotide position	Consequence
1	Exon deletion	2768-2860, inclusive	In frame deletion – 33 amino acids removed

These differences may be found separately or together in various combinations in the different human CLASP-3 isoforms

nucleotide numbering
as in Figure 6A



C

FIG. 6

09737246.121300

Exon 60270 - 20370

CGCCGCAGCCGCCGCCGCCGTCGCCGTCGCCGCAGCAGCCATGGCCGAGCGC
CGCGCCTTCGCCCAGAAGATCAGCAGGTAAATATCCGGCGTGGGGCGC

Exon 85360 - 85510

GTTTTTGCTTCTTCATTGTAGAACGGTGGCAGCCGAAGTTAGGAAGCAGATC
TCCGGACAATATAGTGGTTCTCCCAACTGCTCAAAAACCTTAATATTGTTGG
CAATATATCCCATCACACCACAGTAAGTAACGTATTCAAAATATA

Exon 94500 - 94720

TCTTATCCCAACTTTTTACAAAGGTGCCCCCTTACCGAAGCAGTAGATCCAGTG
GATTTGGAAGATTACCTCATTACTCATCCTTTGGCTGTGGATTCTGGGCCTTT
ACGGGATTTGATTGAATTTCTCCAGATGATATTGAAGTTGTTTATAGTCCTC
GGGACTGCAGAACTCTTGTTTCAGCTGTACCTGAAGAAAGGTAAGGAGACAT
TGACTTATT

Exon 94870 - 94980

TATTTTCCTTTTTTAAAATAGTGAAATGGATCCACATGTTAGAGACTGTATAAG
AAGTTATACAGAAGACTGGGCAATTGTCATCAGAAAGTAAGTTATATGTTTA
TTACAA

Exon 100110 - 100290

ATTTATTTAACTTTTTTTCTTTAATAGATATCATAAATTGGGAACAGGATTTAA
TCCCAATACATTAGATAAACAGAAAGAAAGGCCAAAAAGGTTTGCCAAAAACA
AGTTTTTGAATCTGATGAAGCTCCAGATGGCAACAGCTACCAGGATGATCAA
GTAATACTTTTATTCTTAAATAA

Exon 100340 - 100600

ATATTTAATGTTTTGCATGACAGGATGACCTTAAAAGACGTTCAATGTCAATA
GATGATACCCCAAGGGGTAGCTGGGCCTGTAGTATCTTTGACTTGAAAAATT
CACTTCCTGATGCTTTGCTTCCCAATTTACTTGATCGAACTCCAAATGAAGAA
ATAGACCGTCAGAATGATGACCAAAGGAAATCAAACCGTCACAAAGAACTTT
TTGCTTTGCATCCATCACCAGATGAGGTATAGATGTTTGCATATAAAGAA

Exon 100880-101020

TTTTGGTGTTGCTTTTCAATTTGTAGGAAGAACCAATAGAACGGCTTAGTGTT
CCTGATATACCCAAAGAACATTTTGGTCAAAGACTTCTTGTAATAATGCTTATC
ACTCAAGTGAGTATTTATTTCTTTTACTTACAAC

Exon 112010 - 112120

TTTTTCTTCATAAAGGTTTGAAATTGAAATTGAACCCATTTTGGCAAGTTTGG
CITTATATGATGTCAAGGAAAAGAAAAAGGTAAGATTATATAATTTGACCAT
AGTTAT

Exon 113680 - 113880

AAGTTTAACATACTAATATTTTTTAGATTTTCAGAAAACTTTTATTTTGACCTTA
ATTCTGAGCAGATGAAAGGGTTGTTACGTCCACATGTACCACCTGCTGCCATT
ACTACCCTGGCAAGATCAGCAATTTTTTCTATCACTTATCCTTCCCAAGATGT
TTTTCTTGTAATAAAGGTGAGAATAATGTTAAATATATTG

Exon 115020-115160

TTAATCTTAACTTTTTTTGCCTTTGACAGCTAGAAAAAGTCCTACAGCAAGGA
GACATTGGAGAGTGTGCAGAACCATATATGATTTTCAAAGAAGCAGATGCCA
CCAAGGTAGAATGTTATGCTTCTCATTTCGCCAC

Exon 117200 - 117410

ATGTATAAAGTTCTGTTTTGCAGAATAAAGAAAAACTGGAGAACTGAAGAG
TCAAGCAGATCAGTTTTGCCAAAGACTTGGGAAATATCGCATGCCTTTTGCTT
GGACTGCAATCCATTAAATGAATATTGTTAGCAGTGCTGGGAGTTTGGAAAG
AGATTCTACAGAAGTAGAAATCAGTACTGGAGGTAAGAGTGTTTCATACAAA
AC

Exon 123200 - 123396

AAAATGAATTTTTTTTTTAATTCTTTTGTAGAACGAAAAGGGTCTTGGTCAGA
GAGGAGGAATTCTAGTATTGTTGGCAGACGATCACTTGAAAGGACAACAAGT
GGAGATGATGCTTGTAACCTTGACGAGCTTTCGACCAGCTACTCTCACAGTGAC
AAATTTTTTTAAGCAGGTATTGTTCTGTCATGTAGGAATTTT

(Next part of CLASP, starting
GAAGGAGACCGCTTAAGTGATGAAGATCTCTACAAATTCCTTGCTGATATGA
GAAGGCCATCTTCTGTCTTACGGCGACTAAGACCTATTACAG)

CTTTTCCTCTATTATTGAAATCAGGAAGGAGACCGCTTAAGTGATGAAGATC
TCTACAAATTCCTTGCTGATATGAGAAGGCCATCTTCTGTCTTACGGCGACTA
AGACCTATTACAGGTATTTAAAAATTTTGAGTAGAAATGGTTGCA

TTACATTGTTTTTAATATATAATTTGCAGCTCAGCTCAAGATAGACATTTC
CCGCACCTGAAAATCCCCATTATTGCCTAACTCCGGAGCTGCTTCAAGTGAA
GCTTTACCTTGACAGTAGAGTTAGACCTACCAGAGAAATCTTAGAGTTTCCCG
CAAGGGATGTTTATGTTCCAAACACTACTTACAGGTAAGAGATTTTAATTGG
AGAATTCTG

GTATTTACTATCATCTATACTGTTGCTTTCACAGAAATCTTCTCTACATATACC
CTCAGAGTCTTAATTTTGCCAATCGTCAAGGTTCTGCTAGAAATATAACAGTG
AAAGTCCAGTTTATGTATGGAGAGGATCCAAGCAATGCCATGCCGGTAA

[illegible]


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hCLASP4 -----MFPMEDISISVIGRQRRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLNINIVG 41
hCLASP2 -----MLLFPYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVFVKREPSEFWKKRRTVRRVIEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
      . . .

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHV VNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPAKAE EEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7 G-----VPLTEVV EPLDFEDVLLSRPPDAEPGGLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAE NLLVKEACKFYSSQWHV VNYK 120
      ::

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKD E-----SSSLCSQKGGVVIKQG 105
hCLASP5 DDDLDVVF TPKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVYEVD EEDVKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLLQPRECRTTEP-GIPKD-EKLD AQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKD EDDTSSHSSSKGGGGAGGTGVFKSG 180
      :: .      : * .      : : .

hCLASP4 WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDG SYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPA AQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKR SMSI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDG SYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASG DERSGPFEDSND SRRGSGSP 179
hCLASP1 WLYKGNFNSTVNNVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT 239
      : :      : :      : :      : :      : :      : :

hCLASP4 DVVQCPKMRRHAFELKMLDKYSHYLA AE TEQEME EWLITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKG PVTACDFDLRSLQPDKRLENLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQND DQRKSN-----RHKE 234
hCLASP2 GVVQNNKVRRAFELKMQDKSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK 219
hCLASP7 EDTPRSSGASSI FDLRNLAADSLPSLLERAAPEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMNLDLTYFVLAAETESDMDEWIHTLNRILQISPEGPLQGRRSTEL 299
      * : :      : :      : :      : :

hCLASP4 TAQDDETSS----QGAENIMASLERSMHP ELMKYGRETEQLNKL SRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD----EEDAVEIRPVPECPKEHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD----EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD----EQSKLEGSGSGLD SYLPELAKSAREAEIK---LKSES RVKLFYLDPD 272
hCLASP7 LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRI LVKCLSLKFEIE 273
hCLASP1 TDLGLDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTRN MERLNLFSLDPD 359
      .      :      :      : : : :

hCLASP4 VQR LDFS----GIEPDIKP-FEEKCNKRFLVNCHDLTFN ILGQIGDNAKGPPTNVEPFFI 333
hCLASP5 IEPLFAS----IALYDVKERKKI SENFHC DLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS----LALYDVKEKKKI SENFYFDL NSEQMKGLLRPHVPPAAITTLARS AIFSI 333
hCLASP2 AQKLDFS----SAEPEVKS-FEEKFGKRILVKCN DLSFNLQCCVAENEEGPTTNVEPFFV 327
hCLASP7 IEPIFGI----LALYDVREKKKI SENFYFDL NSDSMKGLLRAGH THPAISTLARS AIFSV 329
hCLASP1 IDTLKLQKKD LLEPESVIKPFEEKAAKRIMI ICKALNSNLQGCVTENENDPITNIEPFFV 419
      : :      : :      : :      : :      : :      : :

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hCLASP4	FKSHLESTIYTQVHKFFHHCQLIQS-----GSKEV-----LIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEN-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNFQYQCKTES-----GAQALGNELVKYLSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSSEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREK-----MSQSPTS NFIRSCKNLLNVE	887
...	*::**::**::**::**::**::**::**::**::**::**::**::**::**::**::**::	
hCLASP4	EQVMIQFLPVILMQLEH-----VLTNMT-----EDDVP	824
hCLASP5	RIEPLVFLHLVLDKLEQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSDQHG	775
hCLASP3	QLEPVVRFLHLLLDKLLLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMIAFLPTILNQLEH-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGA FEAMAHVSVSLVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLEK-----VLVQNE-----EDEIT	916
...	::*::**::**::**::**::**::**::**::**::**::**::**::**::**::**::**::	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVYHVFRLEPVQRDVPKSGAPTALLDPRS YHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVFRLPNTYPNSSSPG-PGGLGGSVHYATMARS AVRPASLNLNRSRSLNS	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDI VAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
...	::*::**::**::**::**::**::**::**::**::**::**::**::**::**::**::**::	
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNC SRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSM TILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS N-----	972
...	::*::**::**::**::**::**::**::**::**::**::**::**::**::**::**::**::	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKGHFHEELALQ-----MNVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLP TKLFHEELALQWVVC SGSVRESALQQA WFFFEIMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVSSSAVREAILQHA-----WFFFLQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAIILKSM	995
...	::*::**::**::**::**::**::**::**::**::**::**::**::**::**::**::**::	
Cadherin Cleavage		
hCLASP4	ATYLLEENKIKLHFGQRFPTYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSHRRTRFSDRFMDDIT TIVNVVTSEIAALLVKPQKENEQA EKMNISLAF	970
hCLASP3	VHHLYFNDKLEAHRKSRFPERFMDDIAALVSTIASDIVSRFQKDTEM---VERLNTSLAF	1076
hCLASP2	AQHLIENSKVKLIRNQRFPSYHHAAETVVMNLMPHITQKFGDNPEA---SKNANHSLAV	956
hCLASP7	ALHLLLGQRDLDRKLRFPGRFLDDIT ALVGSVGLVITRVHKDVEL---AEHLNASLAF	999
hCLASP1	AQHLLIDTNKIQLHRPQRFPE SYQNELDNLMVLS DHVIWKYKDALEE---TRRATHSVAR	1052
...	::*::**::**::**::**::**::**::**::**::**::**::**::**::**::**::**::	
hCLASP4	FLKRCCLTMDRGFIENLINDYISGFSPKDP-----KVLAEYKFEFLQ TICNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVENLIRHYCSQLSAKLSNL---FTLISMRLEFLRILCSHEHYLNLNL	1027
hCLASP3	FLNDLLSVMDRGFVESLIKSCYQVSSKLYSLPNPSVLVSLRLD FLRIICSHEHYVTNL	1136
hCLASP2	FIKRCFTFMDRGFVEKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVESLVR AHYKQVATRLQSSPNPALLTLRMEFTRILCSHEHYVTNL	1059
hCLASP1	FLKRCFTFMDRGCFVEMVN NYISMFS S GDL-----KTLCOYKFD FLQEV CQHEHFIPCL	1107
...	::*::**::**::**::**::**::**::**::**::**::**::**::**::**::**::**::	

Cadherin EC motif

hCLASP4	PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGI	LLRETSI	1060
hCLASP5	FFMNADTAPTSP--CPSISSQNSSSSCSFQDQKIASMFDLTSEYRQQHFLTGI	LFTELAA	1085
hCLASP3	PCSLTTPPASPSVSSATSQSSGFSTNVQDQKIANMFELSVFPFRQQHYLAGI	VLTELAV	1196
hCLASP2	PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGI	LLREVT	1052
hCLASP7	PCCPLSPPASPSVSSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGI	LLTELAL	1119
hCLASP1	PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGI	LLREVG	1157
		..: : : : * * * : : *	
hCLASP4	ALQDN----YEIRYTAISVIKNNLLIKHAFDTRYQHKNQQAQIAQLYLPFVGLLEN	IQRL	1116
hCLASP5	ALDAEGEGISKVQRKAVSAIHSLLSSHLDPRCVKPEVKVIAALYLPVGI	IILDALP--	1143
hCLASP3	ILDPDAEGLFGLHKKVINMVHNLSSHSDSPRYSDPQIKARVAMLYPLIGI	IMETVP--	1254
hCLASP2	ALQEFR----EVRLIAISVLKNNLLIKHSFDDRYASRSHQARIATLYLPFGLLI	ENIVORI	1108
hCLASP7	ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLP	PLLSIARDTLP--	1177
hCLASP1	ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQQAQIASLYMP	PLYGMLLDNMPRI	1213
	* : : : : * * * : : * * * : : : :		
hCLASP4	AGRDTLYSCA-----AMPN-S----ASRDEFPCGFTSPANRGS	LSTDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD-----		1162
hCLASP3	-----QLY-----DFTETHNQGRPICIATDD--		1276
hCLASP2	NVRDVSPFPVNAGMTVKDESALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGI	ASPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQRSRLASMLDSDE		1201
hCLASP1	YLKDLYPFTVNTSNQGSRDDLTNGGFQSQTAIKHANSVDTSFSKDV	LSNIAAFSSIAIS	1273
		.. :	
hCLASP4	FQ-NGHGIKREDSRGLIPEGATGFPDQGNLTGEN-----TRQSSTRSSVSQYN	RLDQYE	1213
hCLASP5	-----EEQEGAGAINQVALAIAGNNFNLT-----SGIVLSSL	PKYQYNMLNADT	1208
hCLASP3	-----YESEGSMISQTVAMAIAGTSVPQLTR---PGSFLTSTSGRQHTT	FSAES	1324
hCLASP2	STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSV	VRCDKLDQSE	1227
hCLASP7	-----GEGDIAGTINPSVAMAIAGGPLAPGSR---ASISQGPPTASRAG	CALSAES	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKI	PRPLALIGSTLRFDRLDQAE	1327
	.. : : : : : : : : : : :		
hCLASP4	IRSLLMCYLYIVKMISEDTLTYWNKVSPQELINILILLEVCLFHFYRMGKRNI	ARVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSS	DKVSTQ	1268
hCLASP3	SRSLLICLLWVLKNADETVLQKWFDTLSVLQLNRLLDLLYLCVSCFEYKGK	VFERINSL	1384
hCLASP2	IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDDFTISEVCLHQFYMGKRY	IARNQEG	1287
hCLASP7	SRTLLACVLWVLKNTPEALLQRAWATDLTLPQLGRLLDLLYLCLAAFEYKGK	KA FERINSL	1309
hCLASP1	TRSLLMCFLHIMKTISYETLIAYWQRAPSPPEVSDFFSILDVCLQNFYLGKR	NIIRKIAA	1387
	..: * * : : * : : : : : : : : * * * : :		
hCLASP4	WLSKHFGIDR-----KSQTMPALRNRSQVMQARLQHLSSLESS-----		1311
hCLASP5	VLQKSRDVKAR-----LEEALLRGEGARGEMMRRRAPGNDRFPGLNEN---		1311
hCLASP3	TFKKS KDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ		1430
hCLASP2	LGPIVHDRKS-----QTLFVSRNRTGMMHARLQQLGSLDNS-----		1323
hCLASP7	TFKKS LDMKAR-----LEEAILGTIGARQEMVRRSRERSPFGNPEN-----		1350
hCLASP1	AFKFVQSTQNNGTILKGSNPSCQTSGLLAQWMHSTSRHEGHKQHR	SQTLPIIRGKN-----	1442
		: : :	
hCLASP4	-----FTLNHSSTTEADIFHQALLEGNTATEVSLTVLDTISFF	TQCFTQLL	1359
hCLASP5	--LRWKKEQTHWROANEKLDKTKAE	LDQEALISGNLATEAHLIILDMQENIQASS-ALD	1368
hCLASP3	ENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEANLIILDTLEIV	QTVS-VTE	1489
hCLASP2	-----LTFNHSYGHSDADVHLHQSLLLEANIATEVCLTALDTLSLFT	LAFKNQLL	1371
hCLASP7	--VRWRKSVTHWKQTSRVDKTKDEMEHEALVEGNLATEASLVVLD	TLEIIVQTM-LSE	1407
hCLASP1	--ALSNPKLLQMLDNTMTSNEIDIVHHVDTEANIATEGCLTILDVSL	FTQTHQRQLQ	1500
		..: : : : * * * * * : : :	

hCLASP4 NNDGHNPLMKKVFVDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFCY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIAKFGDLLFEEVEQC FDLCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHC FATQRALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFVDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRADMCAALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTEL CADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
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hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQII IAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQCATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCSSTIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIISVSQLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
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hCLASP4 SRFOESLFI INNFANS DRPMKATAFFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLIDLQ 1539
hCLASP5 EHLRRLRILAYSEEDTAMQMTPTQVEELL CNLSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRLSKTILTYAEEDLELRETTFPDQVQDLVFNLHMILSDTVKMKEHQEDPEMLIDLQ 1664
hCLASP2 TRFQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ 1551
hCLASP7 EHLRRLSKTILTYAEEDMGLRDSTFAEQVQDLMFNLHMILTDTVKMKEHQEDPEMLIDLQ 1582
hCLASP1 SRFQHS LAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLVDLQ 1679
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transmembrane
hCLASP4 YSLAKSYASTPELRKTTWLD SMAKIHVKNGLFSEAMCYVHVAALVAEYIHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLRLTWLQNM AEKHTKKKQYTEAMCLVHAAALVAEYI SMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSN HAEAAQCLVHSAALVAEYI SMLEDR----- 1718
hCLASP2 YSLAKSYASTPELRKTTWLD SMARIHVKNGLLSEAMCYVHVTALVAEYI TRKG----- 1604
hCLASP7 YRIARGYQGPSDLRLTWLQNMAGKHAELGN HAEAAQCMVHAAALVAEYI LLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGLLSEAMCYIHIAALIAEYI LKRGYWKVEKI 1739
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hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVEDTLSPDEDGV 1633
hCLASP3 -----KYLPGVCVTFQNISSNVLEESAVSDDVSPDEEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDEEASMMEDVGMQD----- 1634
hCLASP7 -----RHLPVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPCDSNSLLTTPSGGSMFSGMWPFLSITPNIKEEGA AKEDSGMHD----- 1795
: * : * : : * : *

ITAM
hCLASP4 ---VHYSEEV LLELLEQCVDGLWKAERYEII SEISKLVPIYEKRRFEKLTQVYRTLHG 1679
hCLASP5 CAGQYFTESGLVGLLEQA AELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQA AASFMSAGMYEAVNEVYKVLIP IHEANRDAKKLSTIHGKIQE 1813
hCLASP2 ---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLIPIIYEKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIP ILEAHRDYKKLA AVHGKIQE 1732
hCLASP1 ---TPYNE NILVEQLYMCGEFLWK SERYELIADV NKP IIAVF EKQ RDKKLS DLYYDIHR 1852
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ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKILEVMHTKKRL LGTFFRVAFYGQSFFEEEDGKEYTYKEHKL TGLSEISRLVKIYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFFG-SKFGDLDEQEFVYKEFAITKLP EISHRLEAFYG 1750
hCLASP3 AFSKIVHQSTGWERMFGTYFRVGFFG-TKFGDLDEQEFVYKEFAITKLA EISHRLEGEYG 1872
hCLASP2 -----DFFEDDGKEYIYKEHKL TPLSEISORLLKIYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFFG-AHFGDLDEQEFVYKEFSITKLA EISHRLEEFT 1791
hCLASP1 SYLKVAEVVNSEKRLFG RYRVAFYGQGFEEEDGKEYTYKEHKL TGLSEISORLLKIYA 1912
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FIG. 8
5 of 6

	ITAM	ITAM	
hCLASP4	ERFGTENVKIIQDS	DKVNAKELDPHYAHIQVTVKBYFDDKELTERKTEFERNHNISR	1799
hCLASP5	QCQGAEFVEVIK	DSTPVDKTKLDPNKAYIQITFVEEYFDEYEMKDRVTYFEKNFNLRRFM	1810
hCLASP3	ERFGEDVVEVIK	DSNPVDKCKLDPNKAYIQITFVEEYFDTYEMKDRITYFDKNYNLRRFM	1932
hCLASP2	DKFGSENVKMIQ	DSGKVNPKDLDSKYAYIQVTHVIEFFDEKELQERKTEFERSHNIRRFM	1770
hCLASP7	ERFGDDVVEIIK	DSYPVDKSKLDSQKAYIQITFVEEYFDTYELKDRVTYFDRNYGLRTFL	1851
hCLASP1	DKFGADNVKIIQ	DSNKNVPKDLDPHYAYIQVTVVTEFFEEKEIEDRKTDFFEMHHNINRFV	1972
	: ** : *:::*** *	: .***: *:::*** *	: ** : *:::*** *
		ITAM	DOCK motif
hCLASP4	FEAPYTLSGKKQ	GCIEEQCKRRTILTTSNSFFYVKRIPINCEQQINLKPIDGATDEIKD	1859
hCLASP5	YTTPTFTLEGR	PRGELHEQYRRNTVLTMTMAFFYIKTRISVIOKEEFVLTPIEVAIEDMCK	1870
hCLASP3	YCTPTFTLDGR	AHGEHQFKRKTILTTSMAFFYIKTRVNVTHKEEILTPIEVAIEDMQK	1992
hCLASP2	FEMPFTQTGKR	QGGVEEQCKRRTILTAIHCFYVKRIPVMYQHHTILNPIEVAIDEMSK	1830
hCLASP7	FCTPTPTDGR	AHGEHQHKKRKTLLSTDHMAFFYIKTRIRVCHREETVLTPEVAIEDMQK	1911
hCLASP1	FETPTTLGKKG	HGGVAEQCKRRTILTTSMLFFYVKRIRIQVISQSSTELNPIEVAIDEMSR	2032
	: ** *:::*** *	: .***: *:::*** *	: ** *:::*** *
		Coiled-coil	
hCLASP4	KTAELOKLCSS	TDVDMIQQLKQLQWVSVQVNAGPLAYARAFND	1919
hCLASP5	KTLLQAVAINQ	EPDAKMLQMVLCQSVGATVNQGP	1930
hCLASP3	KTQELAFATHQ	DPADPKMLQMVLCQSVGTTVNQGP	2052
hCLASP2	KVAELRQLCSS	AEVDMIKLQQLKQSVSVQVNAGPLAYARAF	1890
hCLASP7	KTRELAFA	TEQDPPDAKMLQMVLCQSVGPTVNQGP	1971
hCLASP1	KVSELNQLCT	MEVDMISLQQLKQSVSVKVNAGPMAYARAF	2092
	*. : *	* ** : *** *	*. ** ** : *:::*** *
		Coiled-coil	
hCLASP4	DMFRKFIQACS	ALELNERLIKEDQVEYHEGLKSNFRDMVKELSDIIEHQIQEDTMHSP	1979
hCLASP5	LCFKEFIMRCG	EAVEKNKRLITADQREYQELKKNYNKLKENLRPMIERKIPELYKPIFR	1990
hCLASP3	LCFKDFTKRC	EDALRNKNSLIGPVQKEYQRELKGLSSP-----	2090
hCLASP2	EVFRQFVEACG	QALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKTS-	1949
hCLASP7	LCFKDFCKKCE	DALRNKALIGPDQKEYHRELERNYCRLREALQPIILTQRLPQLMAPTP-	2030
hCLASP1	EIFRQFADACG	QALDVNERLIKEDQLEYQEELRSHYKMDLSELSTVMNEQITGRDDL	2152
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		PDZ ligand	
hCLASP4	WMSNTLHV	FCAISGTSSDRGYGSPHYAEV--	2008
hCLASP5	VESQKRDS	FHRSSFRKCETQLSQGS-----	2015
hCLASP3	-----		
hCLASP2	VLPNSLHI	FNAISGTPPTSTMVHGMTSSSSVV	1980
hCLASP7	--PGLRNS	LNRRASFRKADL-----	2047
hCLASP1	GVDQTC	TRVISKATPALPTVSISSSAEV--	2180

FIG. 8
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